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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:41:32 ; Search time 34.55 Seconds
(without alignments)
1600.893 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARSSFQSQIISLTFV.....RSYPEILTKLTLHYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : A_Geneseq_0601.*
- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
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 - 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
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 - 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
 - 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
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 - 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5019	100.0	915	17 AAR86596	A2058 autotaxin pr
2	5019	100.0	915	22 AAY71987	Human melanoma aut
3	4681	93.3	863	22 AAY71988	Human teratocarcin
4	4632	92.3	859	22 AAY71991	Human autotaxin pr
5	4533	90.3	829	17 AAR86578	Autotaxin derived
6	4430.5	88.3	858	22 AAY71997	Rat autotaxin vari
7	4430.5	88.3	858	22 AAY71999	Rat autotaxin vari
8	4429.5	88.3	858	22 AAY71998	Rat autotaxin vari
9	4426.5	88.2	858	22 AAY71986	Rat autotaxin prot
10	4423.5	88.1	858	22 AAY71996	Rat autotaxin vari
11	4422.5	88.1	858	22 AAY71995	Rat autotaxin vari

12	4341	86.5	849	17 AAR86595	N-tera 2D1 autotax
13	4306	85.8	885	22 AAY71989	Rat brain autotaxi
14	4279	85.3	979	17 AAR86580	Autotaxin derived
15	3842	76.5	788	17 AAR86579	Autotaxin derived
16	1955.5	39.0	873	21 AAY83620	Human PC-1 polypep
17	1955.5	39.0	925	16 AAR79148	Human insulin rece
18	1955.5	39.0	925	20 AAY39355	Insulin receptor t
19	1955.5	39.0	925	21 AAR800195	Breast cancer prot
20	1954.5	38.9	873	21 AAY83621	Variant human PC-1
21	646.5	12.9	457	21 AAG31321	Arabidopsis thalia
22	609	12.1	461	21 AAG29474	Arabidopsis thalia
23	609	12.1	465	21 AAG29473	Arabidopsis thalia
24	599	11.9	400	21 AAG29475	Arabidopsis thalia
25	569	11.3	359	21 AAG31322	Arabidopsis thalia
26	512	10.2	453	20 AAY17529	Human secreted pro
27	512	10.2	453	20 AAY02378	Polypeptide identi
28	512	10.2	453	22 AAB90545	Human secreted pro
29	484	9.6	338	21 AAG31323	Arabidopsis thalia
30	467	9.3	440	21 AAB18910	A novel polypeptid
31	465.5	9.3	477	21 AAB24072	Human PRO1107 prot
32	465.5	9.3	477	21 AAY66716	Membrane-bound pr
33	465.5	9.3	477	22 AAB65239	Human secretory pr
34	465	9.3	411	20 AAY34445	Porphyromonas ging
35	465	9.3	428	20 AAY34324	Porphyromonas ging
36	360	7.2	438	21 AAW90962	Human CSGP-2 prote
37	357	7.1	355	19 AAY75859	Human secretory pr
38	357	7.1	355	20 AAY45165	Human secreted pro
39	241.5	4.8	133	21 AAG31319	Arabidopsis thalia
40	200	4.0	92	21 AAG31320	Arabidopsis thalia
41	179	3.6	109	19 AAW52839	Secreted protein e
42	141	2.8	39	21 AAB53540	Human colon cancer
43	134	2.7	111	13 AAR26050	MSF-K130. Synthet
44	134	2.7	182	12 AAR10872	Protein encoded by
45	134	2.7	452	16 AAR80041	Human megakaryocyt

ALIGNMENTS

RESULT 1
ID AAR86596 standard; Protein; 915 AA.

AC AAR86596;

XX 01-JUL-1996 (first entry)

XX A2058 autotaxin protein.

DE XX

DE Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;

KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.

XX Homo sapiens.

OS WO9532221-A2.

XX 30-NOV-1995.

XX 24-MAY-1995; 95WO-US06613.

XX 28-NOV-1994; 94US-0346455.

XX 25-MAY-1994; 94US-0249182.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Krutcz J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX WPI; 1996-020533/02.

XX Autotaxin motility stimulating protein, and DNA encoding it - used

PT in cancer diagnosis and therapy

XX Claim 4; Page 91-94; 112pp; English.

bad date

XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This
 CC sequence represents the full length protein sequence of the A2058
 CC melanoma cell line ATX protein. ATX is an autocrine motility
 CC stimulating protein which is present in cancer cells. ATX stimulates
 CC both random and directed migration of melanoma cells. The tumorous form
 CC of ATX is a secreted protein, while the transmembrane bound form is not
 CC present in tumour cells. The cDNA encoding this sequence can be used in
 CC a vector, to transform cells. The recombinant cells can then be used to
 CC produce the peptide sequences. Antibodies specific for these sequences
 CC can be produced, and can be used in cancer diagnosis and therapy.
 CC Different sites of localisation of the protein are utilised for diagnosis
 CC and prognosis of the stages of tumour progression. The sequences can be
 CC used in treatment methods to advantageously block the activity of the
 CC secreted form of ATX, while having little effect on the membrane form of
 CC ATX.
 XX
 XX
 SQ Sequence 915 AA;

 Query Match 100.0%; Score 5019; DB 17; Length 915;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MARRSFQSCQIISLFTFANGVSTICLGFTHRIKRAEGWEGPPTVLSDSPTNIGSGCK 60
 Db 1 marrrsfqscqiiisltfavgvsciclgftahrikraegwsegpptvlsdspntnigsgck 60
 QY 61 GRCFELQAGPPDCRCNCLCKSYTSCCHDFDELCLKTARGWECTKDRGGEVRNEENACHC 120
 Db 61 grcfelqagppdcrcnclcksytcscchdfdelclktargwectkdrgevrneenachc 120
 QY 121 SEDCLARGDCCTNYQVYCKGESHVWDDCEIKAECFAGFVRPPLIIFSVDFGRASYMK 180
 Db 121 sedclargdcctnyqvycckgeshvwdcceikaecfagfvrpplliifsvdfgrasymk 180
 QY 181 KSKVMPNIEKLSCGTHSPMRPVYPTKTPNLYTLATGLPESHGIVGNSWMDPVFDA 240
 Db 181 kskvmpnieklscgthspmrpvptktpnlytlatglpeshgivgnsmdpvdida 240
 QY 241 TFHLRGKEFNHRWGGQPLWITATKGVKAGTFWVVIPIHERRILILRWLTLPDHER 300
 Db 241 tfhlrgkefnhrwggqplwitatkgvkagtfwvviipherrililrwltlpdher 300
 QY 301 PSYAFYSEQDFSGHKYIGFPGPESSYGSPTPAKPKRKVAPKRRQRPVAPPKRRR 360
 Db 301 psyafyseqdfsgkhyigfpgpeesygspftpakprkrkvapkrqrpvappkrrr 360
 QY 361 KIHRMDHYAETRODKNTNPLREIDKIVQQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
 Db 361 kihrmthyaaetrqdkntnplreidkivgqlmdglkqlkrrcvnifvgdhgmdevtcd 420
 QY 421 RTEFLSNLYNVDDITVLPGTLGRIRKSFNSNAYDKPAIIANLTCKKPDQHFEPYLAQH 480
 Db 421 rteflsnlynvdditvlpgtlgrirksfnsnaydkpaiianltckkpdqhfepylqah 480
 QY 481 LPKRLHYANNRRRIEDIHLLVRRHWVARKPLDVYKKPSGCKFFQDGHGFDKNVSMQVTF 540
 Db 481 lprkrlhyannrriedihllvrrhwvarkpldvyykpsgckffqgdghgfdknvsmqvtf 540
 QY 541 VVGPTFKYTKVPPFENIELYNVMDCLLLGLKAPNNGTHGSLNHLTLNTFRTPMPEEV 600
 Db 541 vvgptfkytkvppfenielynvmcdlllgkpaannngthgslnhlltntfrtpmpeev 600
 QY 601 TRPNYPCIMYLOSDFDLGCTDDKVEPKNLDLNLKRLHTKGSFEERHLLYGRPAVLYRT 660
 Db 601 trpnypcimylqsdfdlgctddkvepknldelnkrlhtkgsfeerhllgrpavlyrt 660
 QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTSKQAEVSSVPDHLTSCVRPDRVSPSPSQNCL 720
 Db 661 rydilyhtdfesgyseiflmllwtsytvskqaeavssvpdhltscvrpdvrvpsfsqnc 720
 QY 721 AYKNDKMSYGFLLPPPYLSSSPEAKYDAFLVTNMVPMYPAPFKRVWNYFORVLVKKYASER 780

Db 721 aykndkmsygfllppylssspeakydaflvtnmvpmypafkrvwnyforvlvkkyas 780
 QY 781 NGVNVISGPIFYDYDGLDHTEDKIKQYVEGSSIPVPTHYIITSCLDFTOPADKCDGP 840
 Db 781 ngvnvisgpifydydglhdtedkikqyvegssipvpthyisitscldfqpdkcdgp 840
 QY 841 LSVSFFILPHRPDNEBSCNSEDSEKSWELMKMHTARVDRDIEHLTSLDFFRKTSYPE 900
 Db 841 lsvsffilphrpdneescnsedesekwveelmkmtarvdrdiehltsldfrktsype 900
 QY 901 ILTLKTYLHYESEI 915
 Db 901 iltlktylhyesei 915

 RESULT 2
 AAY71987
 ID AAY71987 standard; Protein; 915 AA.
 XX
 AC AAY71987;
 DT 28-MAR-2001 (first entry)
 XX Human melanoma autotaxin.
 DE Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; melanoma.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 127..129
 FT /label= RGD_binding_domain
 FT Active-site 201..213
 FT /note= "Autotaxin phosphodiesterase catalytic site"
 FT
 PN WO200068386-A1.
 XX 16-NOV-2000.
 PD
 XX 05-MAY-2000; 2000WO-US12402.
 PF
 XX 07-MAY-1999; 99US-0306979.
 PR (ZYMO) ZYMOGENETICS INC.
 XX Kelly JD;
 PI
 XX WPI; 2001-007397/01.
 DR
 XX
 PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX
 PS Claim 27; Page 105-108; 126pp; English.
 XX
 CC The present sequence is autotaxin isolated from human melanoma
 CC cells. Autotaxin is a glycoprotein cytokine which increases
 CC insulin signalling in adipose tissue by producing substrate for
 CC adenosine receptors, resulting in inhibition of lipolysis,
 CC decreased hepatic gluconeogenesis and serum glucose levels, and
 CC increased insulin sensitivity. It also inhibits differentiation
 CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
 CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
 CC Autotaxin and its analogues are used to stimulate glucose uptake
 CC by cells, particularly to reduce serum glucose levels for
 CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
 CC or generally any condition associated with elevated serum levels
 CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).

Best local similarity 100.0%, FREQ: NO: 0;
Matches 915; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy	1 MARRSFQSCQIISLTFFAVGVSICLGFTAHRKRAEGWEEGPTVLSDSPWTNIGSCK 60
Db	1 marrsfqscqiislfavgvniclgfahrikraegweeepptvlsdspwtnigsck 60

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QY 61 GRCELOEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGHECTKDRGGEVNEENACHC 120
Db 61 grceleagppdrcdnlcksytschdhdclclktarawecckdrcgevrneenachc 120
QY 121 SEDCLARGDCTNTQVVKCGESHVWDDCEIEKAEECPAGFVRPPLIIFSDGPRASYMK 180
Db 121 sedclargdctntqvkvckgeshwddceiekaeeapagfvrpplifsvdgrfrasymk 180
QY 181 KGSVMPNIEKLSCGTHSPYMRPVYPTKFPNNLYTLATGLYPESHGIVGNSMYDPPVDA 240
Db 181 kgskvmnieklscgthspymrvpyptkfpnnlytlatglypeshgivgnsmydpvda 240
QY 241 TFHLRGKEKNHRWGWGQPLWITATKGVKAGTFFWVPIHERRILITLWLLPLDHER 300
Db 241 tfhlrgkeknhrwggqpwlwitatkgvkgagtffwvpiherrililtlwlpldher 300
QY 301 PSVAFYSEQPDFGSHKYGFPPESSYSGPFTPAKRPKRKVPAPKRRKR 360
Db 301 psyafyseqpdfgshkygfppe----- 324
QY 361 KIRMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKRRVCNVIFVGDHGMEDVTC 420
Db 325 -----ntnplreidkivgqlmdglkqlkhrvcnvifvgdhgmedvtdc 368
QY 421 RTBELSYLNTWDDITILVPGTLGRIRSKFSNNAKYDKAIITANLTCKPDQHFRLKQH 480
Db 369 rteflsnylnvdditilvpgtlgrirskfsnnakypdkaiitanltckpdkqhfrylkqh 428
QY 481 LPKRLHANNRRIEDIHLVRRWHVARKPLDVYKFGSGCFFOGDGHGFDKNVNSMQVNF 540
Db 429 lprlhyannrriedihllverwhvarkpldvkykfgsgcfffogdghgfdknvnsmqv 488
QY 541 VGXGPTFKYKTKVPPFENIELYNVMDLGLKAPNNGTHGSLNHLRTNTFRPTMPBEV 600
Db 489 vgygptfkytkvppfenielynmvmdlglkapnngthgslnhlrrtntfrptmpeev 548
QY 601 TRNYPGIMYLOSDFDLGCTDDKVEPKNKLDENKRLHTKGSSTEERHLLYGRPAVLRYT 660
Db 549 trnypgimylqsdfldgctddkvepknkldelnkrlhtkgssteerhlllygrpavlyrt 608
QY 661 RYDILYHDTFESGYSEIFLMLLWTSYVSKQAEVSSVPDHLTSCVRPDRVYSPFSQCL 720
Db 609 rydilyhdtfesyseiflmlwtsytskqaeavssvpdhltsvrvpdrvyspsfsqcl 668
QY 721 AYKNDKQMSYGFLLPPLSSPEAKYDAFLVNNVMPYPAKRWNNYQORVLVKYASER 780
Db 669 aykndkqmsygfllpplssspeakydaflvnmvmpypakrwynyqorvlvkyaser 728
QY 781 NGVNVISGPIFDYDGLHDTEDKIQYVEGSSIPVPTHYYSITSCLDFTQPADKCDGP 840
Db 729 ngvnvisgpifdydgldhtedkikyvegssipvpthyysitscldftqpdkcdgp 788
QY 841 LSVSSFTLPHRPDNEESCNSDESKVWEELMKMHTARVRDIEHLTSLDFFRKTSRSY 900
Db 789 lsvssfthlphrpndeesncsdeskwweelmkmtarvrdrdiehltsldffrktsr 848
QY 901 ILTKLYLHYEESI 915
Db 849 iltklylhyesei 863

RESULT 4
ID AAY71991
XX AAY71991 standard; Protein; 859 AA.
AC AAY71991;
XX AAY71991;
DT 28-MAR-2001 (first entry)
DE Human autotaxin protein.
XX Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
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KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Domain 8..26
FT /note= "Putative transmembrane domain"
FT Cleavage-site 44..45
FT Binding-site 123..125
FT /label= RGD_binding_domain
FT Active-site 197..209
FT /note= "Putative phosphodiesterase active site"
XX
PN WO200068386-A1.
XX
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US12402.
XX
XX 07-MAY-1999; 99US-0306979.
XX (ZYMO ) ZYMOGENETICS INC.
XX Kelly JD;
XX
XX WPI; 2001-007397/01.
XX N-PSDB; AAD02133.
XX
XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
XX obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX Claim 27; Page 119-121; 126pp; English.
XX
XX The present sequence is human autotaxin protein.
XX Autotaxin is a glycoprotein cytokine which increases
XX insulin signalling in adipose tissue by producing substrate for
XX adenosine receptors, resulting in inhibition of lipolysis,
XX decreased hepatic gluconeogenesis and serum glucose levels, and
XX increased insulin sensitivity. It also inhibits differentiation
XX of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
XX triphosphatase (ATPase) and ATP pyrophosphatase activities.
XX Autotaxin and its analogues are used to stimulate glucose uptake
XX by cells, particularly to reduce serum glucose levels for
XX treatment of non-insulin dependent diabetes (NIDDM) in humans,
XX or generally any condition associated with elevated serum levels
XX of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
XX Transgenic animals that overexpress autotaxin are models for
XX human metabolic diseases.
SQ Sequence 859 AA;
```

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Query Match 92.3%; Score 4632; DB 22; Length 859;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 848; Conservative 3; Mismatches 2; Indels 52; Gaps 1;
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QY 11 QIIISLTFVAVGSICLGFTAHRKRAEGWEGPPVVLSDSPWTNISGSKGRCFELQAG 70
Db 7 riisltfavgvniclgtfahrikraegweegpvtvlstdspwtnsgskgrcfelqag 66
QY 71 PPDRCRDLNCKSYTSCCHDFDELCLKTARGWECTKDRGGEVNEENACHCEDCLARGDC 130
Db 67 pddrcrdnlcksytschdhdclclktargwectkdrgevrneenachcsedclargdc 126
QY 131 CTNYQVVKGESHVWDDCEIEKAEECPAGFVRPPLIIFSDGFRASYMKSGVMPNIE 190
Db 127 ctnyqvkvckgeshwddceiekaeeapagfvrpplifsvdgrfrasymksgvmpnie 186
QY 191 KURSCGTHSPYMRPVYPTKFPNNLYTLATGLYPESHGIVGNSMYDPPVDTAHLRGRKF 250
Db 191 kurscgthspymrvpyptkfpnnlytlatglypeshgivgnsmydpvdtahlrgrkf 250
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Db 541 pknldelnlrhlkgsteerhlllygrpavlrytrydilyhtdfesgyseiflmlwtst 600
 QY 687 TVSKQAEVSVDPHLSVCVRDVRVSPFSONCLAYKNDKQMSYGFLLPPVLSSSPEAKY 746
 Db 601 tsvkqaevsdpdhltsvcvrdrvsvpsfqnclyakndkqmsygfllppvlssspeaky 660
 QY 747 DAFVTVNMPYPAFKRWNYFORVLVKKYASERNGVNVISGPIFDYDGLHDTEDKIK 806
 Db 661 dafvtnmvpmpafkrvnyfgvlyvkkyserngnvvisgpifdydygdghdtedkik 720
 QY 807 QYVEGSSIPVPTTHYSITSCDFTQPADKCDGSLVSSFTLPHRPDNEESCNSSEDESK 866
 Db 721 qyvegssipvptthysitscldftqpadkcdgslsvssfilphrpdpneescnsedesk 780
 QY 867 WVEELMKMTARVRDIBHLVSLDFFRKTSSYPBELTLKTYLHYESEI 915
 Db 781 wveelmkmtarvrldiehltsldffrktssypeliltiktylhyesei 829
 RESULT 6
 AAY71997
 ID AAY71997 standard; Protein; 858 AA.
 AC AAY71997;
 XX AAY71997;
 XX 28-MAR-2001 (first entry)
 DT Rat autotaxin variant (S236T).
 DE
 DE Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
 OS Rattus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 236
 FT /note= "Wild type Ser substituted by Thr"
 FT
 XX WO200068386-A1.
 XX 16-NOV-2000.
 XX
 XX 05-MAY-2000; 2000WO-US12402.
 XX
 XX 07-MAY-1999; 99US-0306979.
 XX (ZYMO) ZYMOGENETICS INC.
 XX PA
 XX Kelly JD;
 PI
 XX WPI; 2001-007397/01.
 XX
 XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 PT
 XX Disclosure; Page -: 126pp; English.
 PS
 XX The present sequence is variant (S236T) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic
 CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated

CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (AAY71986).
 XX
 SQ Sequence 858 AA:
 Query Match 88.3%; Score 4430.5; DB 22; Length 858;
 Best Local Similarity 88.7%; Pred. No. 0;
 Matches 803; Conservative 30; Mismatches 19; Indels 53; Gaps 2;
 QY 11 QIISLFTAVGVSGICIGFTTAHRIKRAEGWEGPPTVLSDSPWNTISGSGKRCFELQEAQ 70
 Db 7 rvislftavgvsgicigfttaasikrae-wdegptvlsdswntntsgsckrcfelqevg 65
 QY 71 PDCRCNLCYSYSCCHDFDELCLKTARGWECTKDRCGEVNEENACHSCSEDCLARGDC 130
 Db 66 pdcrcnlnlcksyscschdfdelclktargwectkdrcevrneenachscsedclsrqdc 125
 QY 131 CTNYGVCKGESHVDDDCCEIEKAAECFAGFVRPPLIIFSVDFRASVMKSKVMPNLE 190
 Db 126 ctnygvckgeshwdddcceelkvpcepagfvrppllifsvdfgrasvmkkskvmnpnie 185
 QY 191 KLRSGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATPHLRGKEF 250
 Db 186 klrsgthapmrpyptktfplnlytlatglypeshgvngsmypdvdfatphlrgref 245
 QY 251 NHRWGGPDLWTATKQGVKAGTFVSVVPIHERRILTLRLWTLTPDHERPSVYAFYSQ 310
 Db 246 nhrwggpdlwtatkqgvragtffvswsipherriltllqlwslpdpnerpsvafyseq 305
 QY 311 PDFSGHKYCPGPESSYSGSPFTPAKPKRKYAPKRRQERPVAPPKRRKTRMDHYAA 370
 Db 306 pdfsgkhypgpe----- 319
 QY 371 ETRQDKMTNPLREIDKIVGOLMDGLKQLKLRVCNVIVFGDHGMEDVTCDRTEFLSNYLT 430
 Db 320 -----mtnplreidktvgqlmdgikqlrlhrcvnnvifvgdhgmedvtdrteflsnlyt 373
 QY 431 NVDDITLVPGLTGRIRSKFSNNAKYDPKAIANLTCRKPQDHFKPKYLKQHLKRLHYANN 490
 Db 374 nvdditlvpgtlgriraksinnskydpkaiantlckkpdqhfkykqlhrlhyann 433
 QY 491 RRIEDIHLLVERHWARKPLDYKKPKSCCFQGDHGFNDKVNMQTVFVGYGPTFKYK 550
 Db 434 rriedihllvrhwarkpldykkpksckcfqgdhgfndkvnsmqtvfvgypgptfkyr 493
 QY 551 TKVPPFENIELYNVCMDDLGLKAPNNGTHGSLNHLRTNTFRPTMPEVTRPNYPGIMY 610
 Db 494 tkvppfenielynvmcdllglkapungchgslnhlrrtntfrptmpevtrpnypgimy 553
 QY 611 LQSDFDLGTCCDDKVEPKNKLDELKRLHKTGSTEERHLLYGRPAVLYRTRYDILYHTDF 670
 Db 554 lqsefdlgtccddkvepknkleeelnrlhktgsteerhlllygrpavlyrtrydilyhtdf 613
 QY 671 ESGYSEIFLMLLWTSYTVSKQAEVSVDPHLSVCVRDVRVSPFSONCLAYKNDKQMSY 730
 Db 614 esgyseiflmlwtstytskqaevsdpdhltsvcvrdrvsvpsfqnclyakndkqmsy 673
 QY 731 GLFFPPYLSSSPEAKYDAFLVTNMPYPAFKRWNYFORVLVKKYASERNGVNVISGPI 790
 Db 674 glffppyssspeakydaflvtnmvpmpafkrvnyfgvlyvkkyserngnvvisgpi 733
 QY 791 FDYDGLHDTEDKIKQYVEGSSIPVPTTHYSITSCDFTQPADKCDGSLVSSFILPH 850
 Db 734 fdyndglrdtedekikyvegssipvptthysitscldftqpadkcdgslsvssfilph 793
 QY 851 RPDNEESCNSSEDESKWVEELMKMTARVRDIBHLVSLDFFRKTSSYPBELTLKTYLHT 910
 Db 794 rpdnecnsedeskwwveelmkmtarvrldiehltsldffrktssypeliltiktylht 853

[illegible]

Qy	191	KLRCGTHSYMPRPVPTKTFPNLYTLATGLYPESHGIVGNSMYDVPDATHLRGREK	250
Db	186	klrscgthsympRPVPTKTFPNlyTLatGLYPeshgIvGnsMYdVPdATHlrgREk	245
Qy	251	NHRWGGQPLWITATKQGVKAGTFFNSVVIPEHRRILITILRWLTLDPOHERPSVAYYSQ	310
Db	246	nhrwggqplwITatKgvKagTffNSvVIpEhrrIlTIlqWlSlpDnErpsvAYySeq	305
Qy	311	PDFSGHYKGFPGPESSYSGSPFPAKRPRKVKAPKRQRPVAPPKKRRKKIHRMDHYAA	370
Db	306	pdfsgHyKgfPgPeSSySGsPFpAKRPRkVKaPRQRpVAPPkKRRkKIhRMDHYAA	319
Qy	371	ETRODKMTPNPLREIDKITVQGLMDGLKQKLLRRCNVNIFVGDHGMEDVTCDRTEFLSNYLT	430
Db	320	-----mtnplreIdKItvgLMDGLkQKlLRrcNVNIFvGDhGMEDvTCdRTEfLSNyLT	373
Qy	431	NVDITLVPGLGIRISKFSNNAKYDPKALIANLTCKKPDQHPKPYLKOHLPKRLHYANN	490
Db	374	nvdItLvpGLgIRIsKfSnnAKyDPkAlIAnLTcKkPDQhPKpYlKOhLPkRLHyann	433
Qy	491	RRIEDIHLVERHWARKPLDVYKKPSGRCFFQGDHGFNDKVNSMQTVFVGVPFPFKY	550
Db	434	rrieDIhLlVErHwArKpLdVYkKpSGrCFFqGDhGFndKvNSMQTVfVGvPFPfKY	493
Qy	551	TKVPPFENIELYNMCDLLGLKPAPNNGTHGSLNHLRTNTFRTPMPEEYTRPNYPGIMY	610
Db	494	tkvppfEnIeLYnmCdLLgKpApNngThGSlnHLrTNTfRTPmPEeYTRpNyPgImy	553
Qy	611	LQSDFDLGCDDKVEPKNKLDLBNKRLHTKGSTEBRHLLYGRPAVLVYRTRVDILYHTDF	670
Db	554	lqSfdlGctcDdkVepKnKlEeLnKrlhTkgStEerHllyGrPaVlVYrTrVdIlYhtdf	613
Qy	671	BSGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDRVSPFSQNCILAYKNDKQMSY	730
Db	614	esgyseIfLmPlWtsYtVskQaEvSSIpEhLtcvRpDrVrSpfSqncIlayKndkQmsy	673
Qy	731	GFLFPPLSSSPEAKYDAFLVTNNMPYPAFKRWNYFORVLVKKYASERNGVNVSIGPI	790
Db	674	gflfPpYlSSsPeaKyDaFlVtNmMpYpAFkRWnyFORvLVkKyASerNgvNvSIgpi	733
Qy	791	PDYDGLHDTEDKIKQYVGSSIPVPTHYYSITSCLDFTQADKCDGPLSVSSFILPH	850
Db	734	fdYnDglrDtEdIkYvgEssIvpThYySItsClDfTqADkCdGpLsvssFilph	793
Qy	851	RPDNEESCNSDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSPYELTLKTYLHT	910
Db	794	rPdneScnsDEskWveELmKmtArVrdIEhLTsLdFFrKtsrSPyELtLkTyLht	853
Qy	911	YESEI 915	
Db	854	yeseI 858	
RESULT	9		
AAAY71986			
ID	AAAY71986	standard; Protein; 858 AA.	
XX			
AC	AAAY71986;		
XX			
DT	28-MAR-2001	(first entry)	
XX			
DE	Rat	autotaxin protein.	
XX			
KW	Rat;	autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;	
KW	adipocyte;	hypoglycemic; antidiabetic; anorectic; antilipemic;	
KW	therapy;	metabolic disease; obesity; dyslipidemia; serum glucose;	
KW	non-insulin	dependent diabetes mellitus; NIDDM; transgenic animal;	
KW	type I	phosphodiesterase activity; ATP pyrophosphatase activity;	
KW	ATPase;	adenosine-5'-triphosphatase activity.	
XX			
OS	Rattus	sp.	
XX			
FH	Key	Location/Qualifiers	

XX
SO Sequence 858 AA:

Query Match	88.38;	Score	4429.5;	DB	22;	Length	858;
Best Local Similarity	88.7%;	Pred.	No. 0;				
Matches	803;	Conservative	30;	Mismatches	19;	Indels	53;
						Gaps	2;

Qy	11	QIISLFTFAVGVSICLGFTHRIKRAEGWEEGPTVLSDPWTNTSGSGCKGRCFELQAG	70
Db	7	rvslsftfaisvniclghtasrikrae-wdeupptvlspdwtntsgsckgrcfelqevg	65
Qy	71	PPDCRDNLCKSVTSCCHDFDELCLTKTARGWECTKDRGCEVNEENACHCSBDCIARGDC	130
Db	66	ppdcrdnlcksvsychdfdelcltktargwectkdrceveeneenachcsedcislrgdc	125
Qy	131	CTNYQVCKGESHWDDCEEIKAAECBPAGFVRPPLIIFSVDGPRASYMKKGSKVMPNIE	190
Db	126	ctnyqvckgeshwddceeikvpecpagfvrppliiifsvdqgrasymkkgskvmpnie	185

xx	Rat autotaxin protein.
xx	
xx	Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
xx	adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
xx	KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
xx	KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
xx	KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
xx	APase; adenosine-5'-triphosphatase activity.
xx	
OS	Rattus sp.
xx	
xx	Key
FH	Location/Qualifiers

FT	Domain	5..15	
FT		/note= "Putative transmembrane domain"	
FT	Binding-site	122..124	
FT		/label= RGD_binding_domain	
FT	Region	143..158	
FT		/label= Epitope	
FT	Region	149..158	
FT		/note= "This region is specifically claimed in claim 10"	
FT		/label= Epitope	
FT		/note= "This region is specifically claimed in claim 10"	
FT	Active-site	136..208	
FT		/note= "Autotaxin phosphodiesterase catalytic site"	
FT	Region	585..595	
FT		/label= Epitope	
FT		/note= "This region is specifically claimed in claim 10"	
XX	WO2000068386-A1.		
XX	16-NOV-2000.		
XX	05-MAY-2000; 2000WO-US12402.		
XX	07-MAY-1999; 99US-0306979.		
XX	(ZYMO) ZYMOGENETICS INC.		
XX	Kelly JD;		
XX	WPI; 2001-007397/01.		
DR	N-PSDB; AAD02131.		
XX	New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -		
PS	Claim 1; Page 101-104; 126pp; English.		
XX	The present sequence is rat autotaxin protein. Autotaxin is a		
CC	glycoprotein cytokine which increases insulin		
CC	signalling in adipose tissue by producing substrate for adenosine		
CC	receptors, resulting in inhibition of lipolysis, decreased hepatic		
CC	gluconeogenesis and serum glucose levels, and increased insulin		
CC	sensitivity. It also inhibits differentiation of adipocytes.		
CC	Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase		
CC	(ATPase) and AMP yrophosphatase activities. Autotaxin and its		
CC	analogues are used to stimulate glucose uptake by cells, particularly		
CC	to reduce serum glucose levels for treatment of non-insulin dependent		
CC	diabetes (NIDDM) in humans, or generally any condition associated		
CC	with elevated serum levels of glucose, lipid or free fatty acid		
CC	(e.g. obesity or dyslipidemia). Transgenic animals that overexpress		
CC	autotaxin are models for human metabolic diseases.		
XX	Sequence 858 AA;		
SQ			
	Query Match 88.2%; Score 4426.5; DB 22; Length 858;		
	Best Local Similarity 88.6%; Pred. No. 0;		
	Matches 802; Conservative 31; Mismatches 19; Indels 53; Gaps		
QY	11 QIISLFTFAVGVSICIGFTHAHRKRAEGWEEGPPTVLSDSPMTNTSGSKRCRCELQAG 70		
DB	: : 1: : : : : : : : : : :		
	7 rvislftfaisvniclgtfasrakrae-wdegpptvlstdspmtntsgsckrcrfelqevg 65		
QY	71 PDCRCNLCIKSYTSCCHDFDELCLKTARGWECTKRCGEVNEENACHCSEDCLARGDC 130		
	: : : : : : : : : : :		
DB	66 pdcrcnclckysyscchdfdelclktargwectkrcgevrneenachcseclsrqdc 125		
QY	131 CTNQQVYKCGESHWDCCDEETKAACCPAGFVRPPLIIFSVDFGRASYMKKGSKYMPNIE 190		
DB	126 ctnyqvvcgeshwvddcceekvpcpgagfvrpplliifsvdvgdfasykmkgskympnie 185		
QY	191 KLRSCGTHSPMRVPVYPTTKFPNLYTLATGLYPESHGIVGNSMIDPVDFATPHLRGKEF 250		

Db	186	klrscgthapmrvpyptkftfnlytiatgypeshgivgnsmypvdfasfhlgrefk	245
Qy	251	nhrwmgcoqlwitatkogvragtffwsvvipherriltilrwltpdherpsvayayseq	310
Db	246	nhrwggoplwitatkgvragtffwsvspheriitliqlwlpdnerpsvayayseq	305
Qy	311	pdfshkygpgpessygsfpftakrpkrvapkrqrpvappkrrrrkhrmdhyaa	370
Db	306	pdfsgkhygpgpe	319
Qy	371	etrodkmtnpureidkivqolmdglkolklrrcvnvifvgdghgmedvtcdrtfslnylt	430
Db	320	-----mtnpreidkivqolmdglklrhrvvnvifvgdhgmedvtcdrtfslnylt	373
Qy	431	nvdtditlvpctglrigrskfsnnaaydkpaliaanltckkpdqhfpvylkqhlpkrlhyann	490
Db	374	nvdtditlvpctglrigrskfsnnaaydkpaliaanltckkpdqhfpvylkqhlpkrlhyann	433
Qy	491	rriedihllvrrrwhvarkpldvvykpsgkcfogdghgfnkvnsmqtvfvgypgpkvk	550
Db	434	rriedihllvrrrwhvarkpldvvykpsgkcfogdghgfnkvnsmqtvfvgypgpkvk	493
Qy	551	tkvppfenielynmcdllglkpapnngthgslnhllrtntfrptmpdevsrpnypgim	610
Db	494	tkvppfenielynmcdllglkpapnngthgslnhllrtntfrptmpdevsrpnypgim	553
Qy	611	lospfdlgctcdkvepkndelnlhltkgssteerhlllygrpavilyrttydilyhtdf	670
Db	554	lqsefdlgctcdkvepkndelnlhltkgssteerhlllygrpavilyrttydilyhtdf	613
Qy	671	esgyseiflmltstvtvskqaeysvdpdhltsrvpdrvspfsfsonclaykndkmsy	730
Db	614	esgyseiflmltstvtvskqaeysvdpdhltsrvpdrvspfsfsonclaykndkmsy	673
Qy	731	gflpppylssspeakaydaflvtnvmvmpyafkrwmvnyfqrlyvkkyaserngvnvisgpi	790
Db	674	gflpppylssspeakaydaflvtnvmvmpyafkrwmvnyfqrlyvkkyaserngvnvisgpi	733
Qy	791	fdydydglhdtedkikoyvgessipvpthyysitscldftqpadkcdgplsvssfilph	850
Db	734	fdydydglhdtedkikoyvgessipvpthyysitscldftqpadkcdgplsvssfilph	793
Qy	851	rpndeesnsdeskvwveelmkmhtarvrdiehltsldffrktssrypeiltktylht	910
Db	794	rpndeesnsdeskvwveelmkmhtarvrdiehltsldffrktssrypeiltktylht	853
Qy	911	yesei 915	
Db	854	yesei 858	
RESULT 10			
AAAY1996			
ID	AAAY1996 standard; Protein; 858 AA.		
XX	AAAY1996;		
AC			
XX			
DT	28-MAR-2001 (first entry)		
XX			
DE	Rat autotaxin variant (A194V).		
XX			
KW	Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;		
KW	adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;		
KW	therapy; metabolic disease; obesity; dyslipidemia; serum glucose;		
KW	non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;		
KW	type I phosphodiesterase activity; ATP pyrophosphatase activity;		
KW	AtPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant		
OS	Rattus sp.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	


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Db 1 marqcglsqvislftfaiswniclgftasikrae-wdegpptvlsspwcntsgsck 59
Qy 61 GRCFELQAGPDCRDLNCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
Db 60 grcfelqevgppdcnclckysccchdfdelclktvrgweckdarsgevrneenachc 119
Qy 121 SEDCLARGDCCTNYOVCKGESHWDD-----DCEETKAABECAPAGFVRPPLIIFSVDG 173
Db 120 pedclsrqdcctnyqvckgeshwddaarnqssclqv-----cp-----ppliifsvdg 170
Qy 174 FRASYMKKSGKMPNIEKLRSCTGTHSPYMRPVYPTKTFNLYTLATGLYPESHGIVGNSM 233
Db 171 frasymkkgkmpnieklrscgthvpycrpypptkftfnlytclatglypeshgivgns 230
Qy 234 YDPVDFATFHLRGREKFNHRMGGOPLTATKQGVKAGTFFWVSVPHERRIILTLRLWL 293
Db 231 ydpvdfasfhlrgrekfnhrwggplwtackgvratffwsvipherriiltllqwl 290
Qy 294 TLPDHERSVAFYSEQDPFSCHKYGPFGPDESSYSGSTTPAKRPRKRVAPKRQRERVA 353
Db 291 slpdnerpsvafyseqpdfsghkypfgpe----- 321
Qy 354 PPKRRRRKIRHMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLRRCVNVIFVGDHG 413
Db 322 -----mcnplreidktvgqlmdgkqlrlhrcvnlvifvgdhg 358
Qy 414 MEDVTCDRTEFLSNLYTNVDDITLPGTLGRIRSRFSNNAKYDPKAIANLTKCKPDQHF 473
Db 359 medvtdcrtelfsnlytnvdditlpgtlgriraksinnskypdktianlctckpdqhf 418
Qy 474 KPYLKQHLPLKRLHYANNRRIEDHLLVERHWVARKPLDYKKPSCKCFQGDHGFQNKV 533
Db 419 kpymkqlhplkrlhyannrriedihllvdrwhvarpldykkpsckcfqgdhgfndkv 478
Qy 534 NSMOTVFYGYGPTFKYKTKVPFENELYNVMCDLLGLPAPNNGTHGSIHLHRTNTPR 593
Db 479 nsmqctvfygygptfkkyrtkvpfenelynvmcdllglpapgngthgshlhlrtntfr 538
Qy 594 PTMPPEVTRPNYPGIMYLQSDPDLGCTCDKVEPKNKLDELNKLRLHTKGSTE----- 645
Db 539 ptmpdevsrpnypgimylqsefdlgtcdcdkvepknkleeelnkrlhtkgssteaetkfrg 598
Qy 646 -----ERHLLYGRAVLYRTRYDILYHTDFESGYSEIFLMLLTSTYV 698
Db 599 skhenknlngsvpekrhlllygpavlyrtsydilyhtdfesgyseiflmlplwtsyti 658
Qy 689 SKQAEVSSVPDLHTSCVRPDVRSFSONCLAYKNDQKMSYGFLEPPYLSSSPKAKYDA 748
Db 659 skqaevsipsehltncvrpdvrvspgfsqnclyakndkmsygfifppylssspeakya 718
Qy 749 FLVTNMVPMYPAFKRWVNYFORVLVKYASERNGVNIVSGPIFDYDGLHDTEDKIKOY 808
Db 719 flvtnmvpmypafkvwayfqrvlvkkyaserngvnvisgpifdynyldrtdedeikqy 778
Qy 809 VEGSIPVPTHYIITSCLDPTQPADKCDGPLSVSSFFILPHRPDNEESCSEDESKW 868
Db 779 vegsipythysliitscldtqpadkcdgplsvssffilphrpndescnsedeskvw 838
Qy 869 EELMKMHTARVDIEHLSLDFRKTSSYPREILLKTYLHYESEI 915
Db 839 eelkmkhtarvrdiehlsgldfyrktsrsyseilktilyhesai 885

```

RESULT 14

AA86580
ID AA86580 standard; Protein; 979 AA.

XX AC AA86580;

XX DT 28-JUN-1996 (first entry)

XX DE Autotaxin derived from human liver cells.

```

XX Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 864 /note= "unspecified amino acid"
FT Misc-difference 889 /note= "unspecified amino acid"
FT Misc-difference 903 /note= "unspecified amino acid"
FT Misc-difference 911 /note= "unspecified amino acid"
FT Misc-difference 927 /note= "unspecified amino acid"
FT Misc-difference 937 /note= "unspecified amino acid"
FT Misc-difference 944 /note= "unspecified amino acid"
FT Misc-difference 950 /note= "unspecified amino acid"
FT Misc-difference 954 /note= "unspecified amino acid"
FT Misc-difference 967 /note= "unspecified amino acid"
FT Misc-difference 975 /note= "unspecified amino acid"
XX WO9532221-A2.
XX 30-NOV-1995.
XX 24-MAY-1995; 95WO-US066613.
XX 28-NOV-1994; 94US-0346455.
XX 25-MAY-1994; 94US-0249182.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Krutcz J, Liotta L, Murata J, Schiffmann E, Stracke M;
XX WPI; 1996-020533/02.
XX Autotaxin motility stimulating protein, and DNA encoding it - used
XX in cancer diagnosis and therapy
XX Claim 4; Page 67-70; 112pp; English.
XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is
XX an autocrine motility stimulating protein which is present in cancer
XX cells. ATX stimulates both random and directed migration of melanoma
XX cells. The tumorous form of ATX is a secreted protein, while the
XX transmembrane bound form is not present in tumour cells. The cDNA
XX encoding this sequence can be used in a vector, to transform cells.
XX Antibodies specific for these sequences can be produced, and can be used
XX in cancer diagnosis and therapy. Different sites of localisation of the
XX protein are utilised for diagnosis and prognosis of the stages of tumour
XX progression. The sequences can be used in treatment methods to
XX advantageously block the activity of the secreted form of ATX, while
XX having little effect on the membrane form of ATX.
XX Sequence 979 AA;

```

Query Match 85.3%; Score 4279; DB 17; Length 979;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;

QY 1 MARRSSQSCQIISLFTFAVGVSICLGTFAHRAEGWEGPPTVLSDSPWTNIGSCK 60
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db	1	marssfqscqdisl1ffavgvnicl1gftahrikraegweegpvtvlsdspwtinsgsk	60
Qy	61	GRCFELQEAGPPDCRDNLCCKSYTSCCHDFDELCLTKTARGWECTKDRCGEVNEENACH	120
Db	61	grcfelqeagppdcrcdnlccksytschdfdelcltktargwectkdrcevneenach	120
Qy	121	SECLARGDCCTWYQVCKGESHWVDDDEEIKAAECFAGFVRPPLIIFSVDGF--RASY	178
Db	121	sedclargdcctwnyqvckgeshwvdddeekaaecf--vcspsinhllgwlpmtsy	178
Qy	179	MKKGSKVMPNIEKLRCGSHSPYMRVYPTKTPNLYTLATGLYPESHGIVGNSMYDPVF	238
Db	179	mkkgskvmpnieklrscgshspymrvyptktpnlytlatgypeshgilvgnsmvdpvf	238
Qy	239	DATFHLRGREKFNHRWGGGLOPLWITATKGVKAGCTFFWSVI----PHERRIULTILRWLT	294
Db	239	datfhlgreknhrwgggplwitatkgres----wvllvcehpsraeiltllqlwt	294
Qy	295	LPDHERPSVYAFYSEQPDFSGHKYGFPGPEESSYSGSFTPAKRPKRKVAPKRRQERPAP	354
Db	295	lpdherpsvyafyseqpdfsgkhmpfge-----	324
Qy	355	PKRKRRIHRMDHYAAETRODKMTNPLREIDKIVGOLMDGLKQLKLRVCNVVIFVGDHOM	414
Db	325	-----mtnprenmhkivggldgklqklhrccnvivf--et	359
Qy	415	EDVTCD--RTEFLSNLYTNVDDTLTPGTLGRTRSFNSNAKYDPAKIAIANITCKKPDQH	472
Db	360	mdgrchmyrteflsnlytnvddtltpgltlgrlrsfnakaydpkaiianitckkpdqdn	419
Qy	473	FKPYLAKOHLPKRLHYANNRRIDIEHLLVERRHWARKPLDVYKKPSGCKFFQCDGHGFDNK	532
Db	420	fkpylkqhlpkrlhyannrriedihllverhwarckpidvykkpsgnafrettafdnk	479
Qy	533	VNSMQTVFVYGTFYKTKVPFPFENIELYNVMDLLGLKAPANNTHGSLNHLRTNTFF	592
Db	480	vnsmqtvfvyggtfkytkvpfenielynvmcdllgikpappingthgslnhllrntff	539
Qy	593	RPTMPREVTNPYVGTMYLQSDRDLGCTCDDKVEPKNKLDENKRLHRTKGSTFEERLLYG	652
Db	540	rptmpeevtrpnypgmylqsdldlgctcddkvepknkldelnkrlhtkgsteerhlyyg	599
Qy	653	-RPAVLYRTRYDILYTHDFESGYSEIFLMLLWTSYVSKQAEVSSVPDHLTSCVRPDVRV	711
Db	600	drpavlyrtrydilythdfesgyseiflmlwtsyvsqkqaevsyvpdhltsvrvpdrv	659
Qy	712	SPFSQNCLAYKNDKQMSGYFLPPPYLSSSPEAKYDAFLVTNMVPMYPAFVRWVNYFQRV	771
Db	660	spsfsgncalaykndkqmsygfllppylssspeakydafivtnmvpmypafkrwvnyfqr	719
Qy	772	LVKKYASERNGVNISGPIFDYDGLHTEDEKIKOYVEGSSIPVPTHYYSITSLDFTF	831
Db	720	lvkkyaserngvnisgpifdydgldhtedekikoyvegssipvpthyysitscldft	779
Qy	832	QPADKCDGPLSVSFFILPHRPDNEESCNSDESKVVEELMKMHRTARVDIEHLTSLDFF	891
Db	780	qpadkcdgplsvsffilphrpdnecnsdeskvwveelmkmhrtarvrdiehltsldff	839
Qy	892	RKTSRSYPEILTKLYLHYESES1	915
Db	840	rktrsrypeiltklylhyese1	863
RESULT 15			
AAR86579			
ID	AAR86579 standard; Protein; 788 AA.		
XX	AAR86579;		
AC			
XX			
DT	28-JUN-1996 (first entry)		
XX			
DE	Autotaxin derived from teratocarcinoma N-tera 2D1 cells.		
XX			

KW	Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW	melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX	
OS	Homio sapiens.
XX	
PN	WO9532221-A2.
XX	
PD	30-NOV-1995.
XX	
XX	24-MAY-1995; 95WO-US06613.
XX	
XX	28-NOV-1994; 94US-0346455.
PR	25-MAY-1994; 94US-0249182.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
XX	
DR	WPI; 1996-020533/02.
DR	N-PSDB; AAT06613.
XX	
PT	Autotaxin motility stimulating protein, and DNA encoding it - used
XX	in cancer diagnosis and therapy
PS	Claim 4; Page 62-65; 112pp: English.
CC	
CC	AA86959-R86596 represent autotaxin (ATX) and fragments of it. ATX is
CC	an autocrine motility stimulating protein which is present in cancer
CC	cells. ATX stimulates both random and directed migration of melanoma
CC	cells. The tumourous form of ATX is a secreted protein, while the
CC	transmembrane bound form is not present in tumour cells. The cDNA
CC	encoding this sequence can be used in a vector, to transform cells. The
CC	recombinant cells can then be used to produce the peptide sequences.
CC	Antibodies specific for these sequences can be produced, and can be used
CC	in cancer diagnosis and therapy. Different sites of localisation of the
CC	protein are utilised for diagnosis and prognosis of the stages of tumour
CC	progression. The sequences can be used in treatment methods to
CC	advantageously block the activity of the secreted form of ATX, while
CC	having little effect on the membrane form of ATX.
XX	
SQ	Sequence 788 AA;

	Query Match	76.5%; Score 3842; DB 17; Length 788;
	Best Local Similarity	85.6%; Pred. No. 0;
	Matches	727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;
Qy	76	CDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVNRNEENACHCSEDLARGDCCTNYQ 135
Db	1	cdnlcksytscchdfdelclktarawectkrcgevrneenachcseclargdctnyq 60
Qy	136	VVKGESHWDDCEEIKAAECPAGFVRPPILIFSVDFG- -RASYMKSGSKVMPNIEKLRL 193
Db	61	vckgeshwddceelkaaeclq- -vdpslnhlrlgwlpmtsymksgskvmpnaeklr 118
Qy	194	SCGRHSPYMRPVYPTKTPNNLYTLATGLYPESHIGIVGNSMDVPDFAFHLRGREKFNHR 253
Db	119	scgrthsypmrpyptkttfplnlytlatglypeshigivansmydpvfdaufhlgrekfnhr 178
Qy	254	WWGOPLMITATKGCVKAGTFWSVI- - -PHERRILTILRWLTLPDHERPSVYAFYSE 309 : :
Db	179	waggplwitatkgres- - -wnillvcchpstaeililiqltpdherpsvyafyse 234
Qy	310	QPDPSGHKYGPFGPESSYGSFFPAKPAPKKRVAPKRQRPVAPPKRRRIHRMDHYA 369 : :
Db	235	qpdfsghkhmfpge- 249
Qy	370	AETRODKMTNPRLRETDKIVGOLMDGLKOLKLRCCVNVI FVGHDGMEDVTCD- - RTEFLSN 427 : :
Db	250	- - - - - - - - - - - mnpnlrennhkvvgimogikgklhrcvnvifv- - - etmdgrchmyrteflsn 299
Qy	428	YLTVNDDTITLVPGTLGRIRSRFSNNAKYDPRAITANLTKCPDQHFKPYLKPHLPKRLHY 487

Db 300 yltnvdditclvpgtlgrirskfsnnakypkaiianltckkpdqghfkpylkqhlprlhy 359
Qy 488 ANNRRIEDIHLLVERHWVARPLDVIYKKPSGKCFQGDHGFQDNKVNMQTVFVGYPTE 547
Db 360 annrriedihllverhvarpdlvdkpvggnafarettafdknkvnsmqtvfvgypTF 419
Qy 548 KYKTKVPPPEINELNVNMCDDLGLKLPAPNNGTHGSLNHLRTNTERPTMEEVTRNYPG 607
Db 420 kytkvpprenlelynvnmcdllglkpapngthfslnhlrtntfrptmpeevtrpnypg 479
Qy 608 IMYLSQDFDLGCTCDDKVBPKNKLDLNLKRLHTKGSTEERHLLYG-RPAVLYRTRYDILY 666
Db 480 imylqsdfalgctcdkvepknlgeInkrlhtkgssteerhlllygdrpavlyrtrydily 539
Qy 667 HTDFESGYSEIFMLMLWTSYTVSKQAEVSSVPDHLTSCVRPDVRSFSPSQNCLAYKNDK 726
Db 540 htdfesgyseiflmpIwtsytvskqaeVssvpdhlTscvrdvrvspsfsqncIaykndk 599
Qy 727 QMSYGFLEPPYLLSSPEAKYDAFLVTNMYPMYPAPKRVNYPFORVLVKKYASERNGVNVI 786
Db 600 qmsygglgppylssspeakydaflvtnmvmpypafkrvwnyfqrvlvkkyaserngvnvi 659
Qy 787 SGPIFDYDGLHDEDKIKQYVEGSSIPVPTHYYSIIITSCLDFTQPADKCDGPLSVSSF 846
Db 660 sgpfidydydglhdedkikqyvegssipvpthyysIItscldftqpadkcdgplsvssf 719
Qy 847 ILPHRPDNEESCNESESKWVEELMKMHTARVRDIEHLTSLDFFFRKTSRSPYEILTlKT 906
Db 720 ilphrpdneescnsedeskwweelmkmhtarvrdiehltsldfcktsrsypeilTlkt 779
Qy 907 YLHTYESEI 915
Db 780 ylhTyeseI 788

Search completed: July 19, 2001, 14:45:00
Job time: 208 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:42:27 ; Search time 20.45 Seconds
(without alignments)
901.337 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSFQSQIISLTFV.....RSYPEILTKLYLHYESEI 915

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5019	100.0	915	1	US-08-346-455B-69
2	5019	100.0	915	3	US-08-977-221-69
3	5019	100.0	915	5	PCT-US95-06613-69
4	4533	90.3	829	1	US-08-346-455B-34
5	4533	90.3	829	3	US-08-977-221-34
6	4533	90.3	829	5	PCT-US95-06613-34
7	4418	88.0	861	1	US-08-346-455B-67
8	4418	88.0	861	3	US-08-977-221-67
9	4279	85.3	979	5	PCT-US95-06613-67
10	4279	85.3	979	1	US-08-346-455B-38
11	4279	85.3	979	3	US-08-977-221-38
12	4279	85.3	979	5	PCT-US95-06613-38
13	3842	76.5	788	1	US-08-346-455B-36
14	3842	76.5	788	3	US-08-977-221-36
15	3842	76.5	788	5	PCT-US95-06613-36
16	1955.5	39.0	873	3	US-09-187-331-6
17	1955.5	39.0	873	5	US-08-392-946-1
18	1955.5	39.0	925	2	US-08-504-169-1
19	1955.5	39.0	925	5	PCT-US94-14893-1
20	360	7.2	438	3	US-09-187-331-2
21	357	7.1	355	2	US-09-014-969-19
22	192	3.8	39	1	US-08-346-455B-54
23	192	3.8	39	3	US-08-977-221-54
24	192	3.8	39	5	PCT-US95-06613-54
25	126.5	2.5	2471	4	US-09-112-450-4
26	123	2.5	4654	4	US-08-476-515A-84
27	123	2.5	4655	4	US-08-652-877-84

28	123	2.5	4655	4	US-08-652-877-88	Sequence 88, Appl
29	123	2.5	4655	4	US-08-652-877-90	Sequence 90, Appl
30	122	2.4	4655	4	US-08-652-877-86	Sequence 86, Appl
31	118	2.4	23	1	US-07-822-043-11	Sequence 11, Appl
32	115	2.3	1833	3	US-08-479-722B-2	Sequence 2, Appl
33	115	2.3	1833	5	PCT-US95-02251-18	Sequence 18, Appl
34	113	2.3	22	1	US-07-822-043-33	Sequence 33, Appl
35	113	2.3	22	1	US-08-346-455B-33	Sequence 33, Appl
36	113	2.3	22	3	US-08-977-221-33	Sequence 33, Appl
37	113	2.3	22	5	PCT-US95-06613-33	Sequence 33, Appl
38	112	2.2	1394	6	517197-30	Patent No. 517197
39	110	2.2	23	1	US-08-346-455B-11	Sequence 11, Appl
40	110	2.2	23	3	US-08-977-221-11	Sequence 11, Appl
41	110	2.2	23	5	PCT-US95-06613-11	Sequence 11, Appl
42	109.5	2.2	1810	5	PCT-US95-11684-4	Sequence 4, Appl
43	108	2.2	465	3	US-08-701-582D-13	Sequence 13, Appl
44	108	2.2	465	3	US-09-063-893A-19	Sequence 19, Appl
45	107.5	2.1	605	4	US-09-042-785A-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-346-455B-69
Sequence 69, Application US/08346455B
Patent No. 5731167
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA: DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434.
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 915
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: CDNA


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; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-346-455B-69

Query Match      100.0%; Score 5019; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSFQSQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWNTNIGSCK 60
Db 1 MARRSFQSQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWNTNIGSCK 60
QY 61 GRCFELQEAAGPPDCRCNLCNLSYTSCHDFDELCLKTARGWECTKDRGGEVRNEENACHC 120
Db 61 GRCFELQEAAGPPDCRCNLCNLSYTSCHDFDELCLKTARGWECTKDRGGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNTQVVCKGESHVDDCEIEKAAECAPAGFVRPPLIIFSVDFGRASYMK 180
Db 121 SEDCLARGDCCTNTQVVCKGESHVDDCEIEKAAECAPAGFVRPPLIIFSVDFGRASYMK 180
QY 181 KGSVMPIEKLRCSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMYDPVDA 240
Db 181 KGSVMPIEKLRCSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMYDPVDA 240
QY 241 TFHLRGREKFNHRWGWGLOPLWITATKQSVKAGTFPWSVVIPIHERRILTLRLWTLDPHER 300
Db 241 TFHLRGREKFNHRWGWGLOPLWITATKQSVKAGTFPWSVVIPIHERRILTLRLWTLDPHER 300
QY 301 PSVYAFYSEQPDFSGHKYGPFGPESSYSGSPFTPAKRPRKRVAPKRRQRPVAPPKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGPFGPESSYSGSPFTPAKRPRKRVAPKRRQRPVAPPKRRR 360
QY 361 KIHRMDHYAAETRODKNTNPREIDKIVQQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
Db 361 KIHRMDHYAAETRODKNTNPREIDKIVQQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
QY 421 RTEPLSNVLTNVDDITLVPGLGRIRSRFSNNAKYDPAKAIANTLCKPKDQHFYKYLKQH 480
Db 421 RTEPLSNVLTNVDDITLVPGLGRIRSRFSNNAKYDPAKAIANTLCKPKDQHFYKYLKQH 480
QY 481 LPKRLHYANNRRIEDIHLVVERRHVAARKPLDVYKKPSGKCFQGDHGFDRKNVSMQTVF 540
Db 481 LPKRLHYANNRRIEDIHLVVERRHVAARKPLDVYKKPSGKCFQGDHGFDRKNVSMQTVF 540
QY 541 VGGPTFKYTKVPPFENIELYNVWCDLLGLKPAPNNGTHGSLNHLTLTNTFRPTMPEEV 600
Db 541 VGGPTFKYTKVPPFENIELYNVWCDLLGLKPAPNNGTHGSLNHLTLTNTFRPTMPEEV 600
QY 601 TRPNYPGIMYLOSDFDLGCTCDDKVEPKNKLDLNLKRLTKGSTERHLLYGRPAVLVYRT 660
Db 601 TRPNYPGIMYLOSDFDLGCTCDDKVEPKNKLDLNLKRLTKGSTERHLLYGRPAVLVYRT 660
QY 661 RYDILYHTDFESGYSEIFLMLLTSTYVSKQAEVSSVPDHLTSCVRPDRVSPFSQNC 720
Db 661 RYDILYHTDFESGYSEIFLMLLTSTYVSKQAEVSSVPDHLTSCVRPDRVSPFSQNC 720
QY 721 AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNVMVPMYPAKRVWNYFORVLVKKYASER 780
Db 721 AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNVMVPMYPAKRVWNYFORVLVKKYASER 780
QY 781 NGVNVISGPIFDYDGLHDTEDKIKQVVEGSSIPVPHYYSILTSCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHDTEDKIKQVVEGSSIPVPHYYSILTSCLDFTQPADKCDGP 840
QY 841 LSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVROIEHTLSLDFFRKTSRSYPE 900
Db 841 LSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVROIEHTLSLDFFRKTSRSYPE 900

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QY 901 ILTLKTYLHTYSEI 915
Db 901 ILTLKTYLHTYSEI 915

RESULT 2
US-08-977-221-69
; Sequence 69, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-977-221-69

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Query Match      100.0%; Score 5019; DB 3; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARRSFQSQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWNTNIGSCK 60
QY 61 GRCFELQEAAGPPDCRCNLCNLSYTSCHDFDELCLKTARGWECTKDRGGEVRNEENACHC 120

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Db 61 GRCFELQAGPPDCRDLNLSKSYTSCCHDFDELCLKTARGWECTKDRCEVNEENACHC 120
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Db 121 SEDCLARGDCCTNYQVCKGESHWWDDCEIEKAAECPCAGFVRPPLIIFSVGDFRASYMK 180
Qy 181 KGSVMPNIEKLRSCGTHSPYRPPYPTKTFPNLTATGLYPESHGIVGNSWMDPVFDA 240
Db 181 KGSVMPNIEKLRSCGTHSPYRPPYPTKTFPNLTATGLYPESHGIVGNSWMDPVFDA 240
Qy 241 TFHLRGREKFNHRWGGQPLWTATKQGVKAGTFWVSVVIPHERRILTLRLWLTLPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWTATKQGVKAGTFWVSVVIPHERRILTLRLWLTLPDHER 300
Qy 301 PSVYAFYSEQDFSGHKYGFPGPESSYSGSPPTAKRPRKRVAPKRRR 360
Db 301 PSVYAFYSEQDFSGHKYGFPGPESSYSGSPPTAKRPRKRVAPKRRR 360
Qy 361 KIRMDHYAAETRODKWNTNPLREIDKIVQLMDGLKQLKRCVNVIFVGDHGMEDVTC 420
Db 361 KIRMDHYAAETRODKWNTNPLREIDKIVQLMDGLKQLKRCVNVIFVGDHGMEDVTC 420
Qy 421 RTEFLSNVLTNVDITLVPGLTGRIRSFNSNAKYDPKAIANLTKCKPDQHFXYLKH 480
Db 421 RTEFLSNVLTNVDITLVPGLTGRIRSFNSNAKYDPKAIANLTKCKPDQHFXYLKH 480
Qy 481 LPKRLHYANNRRIEDIHLLVERRHWVARKPLDVYKKPSGKCFQGDHGFNDKVNMSQTVF 540
Db 481 LPKRLHYANNRRIEDIHLLVERRHWVARKPLDVYKKPSGKCFQGDHGFNDKVNMSQTVF 540
Qy 541 VGYGPTKYTKVPPFENIELYNVMDLLGLKPAFNNNGTHGSLNHLRLTNTFRTPMPEV 600
Db 541 VGYGPTKYTKVPPFENIELYNVMDLLGLKPAFNNNGTHGSLNHLRLTNTFRTPMPEV 600
Qy 601 TRPNYPGIMYLOSDFLGCCTODKVEPKNDLDELNKLHTKSTEEHLLYGRPAVLYRT 660
Db 601 TRPNYPGIMYLOSDFLGCCTODKVEPKNDLDELNKLHTKSTEEHLLYGRPAVLYRT 660
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Db 721 AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVNMVPMYPAFRVWNYFORVLVKYASER 780
Qy 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPHYYSIITSCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPHYYSIITSCLDFTQPADKCDGP 840
Qy 841 LSVSSFILPHRPDNEESCSNSEDSESKWVEELMKMTARVRDIEHLTSLDFFRKTSRYPE 900
Db 841 LSVSSFILPHRPDNEESCSNSEDSESKWVEELMKMTARVRDIEHLTSLDFFRKTSRYPE 900
Qy 901 ILTLKTYLHTYESBI 915
Db 901 ILTLKTYLHTYESBI 915
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RESULT 3

PCT-US95-06613-69

; Sequence 69, Application PC/TUS9506613

; GENERAL INFORMATION:

; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;

; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,

; APPLICANT: HENRY; MURATA, JUN

; TITLE OF INVENTION: MOTILITY STIMULATING

; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND

; TITLE OF INVENTION: THERAPY

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

```
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 915
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: A2058 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06613-69
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Query Match 100.0%; Score 5019; DB 5; Length 915;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MARRSFQSCQIISLFTFAVGSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGCK 60
Db 1 MARRSFQSCQIISLFTFAVGSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGCK 60
Qy 61 GRCFELQAGPPDCRDLNLSKSYTSCCHDFDELCLKTARGWECTKDRCEVNEENACHC 120
Db 61 GRCFELQAGPPDCRDLNLSKSYTSCCHDFDELCLKTARGWECTKDRCEVNEENACHC 120
Qy 121 SEDCLARGDCCTNYQVCKGESHWWDDCEIEKAAECPCAGFVRPPLIIFSVGDFRASYMK 180
Db 121 SEDCLARGDCCTNYQVCKGESHWWDDCEIEKAAECPCAGFVRPPLIIFSVGDFRASYMK 180
Qy 181 KGSVMPNIEKLRSCGTHSPYRPPYPTKTFPNLTATGLYPESHGIVGNSWMDPVFDA 240
Db 181 KGSVMPNIEKLRSCGTHSPYRPPYPTKTFPNLTATGLYPESHGIVGNSWMDPVFDA 240
Qy 241 TFHLRGREKFNHRWGGQPLWTATKQGVKAGTFWVSVVIPHERRILTLRLWLTLPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWTATKQGVKAGTFWVSVVIPHERRILTLRLWLTLPDHER 300
Qy 301 PSVYAFYSEQDFSGHKYGFPGPESSYSGSPPTAKRPRKRVAPKRRR 360
Db 301 PSVYAFYSEQDFSGHKYGFPGPESSYSGSPPTAKRPRKRVAPKRRR 360
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QY 361 KIIRMDHYAAETRODKMTNPLREIDKIVGQIMDGLKQLKLRRCVNVIFVGDHGMEDVTC 420
Db 361 KIIRMDHYAAETRODKMTNPLREIDKIVGQIMDGLKQLKLRRCVNVIFVGDHGMEDVTC 420
QY 421 RTFELSNLYTNVDDITLVPGTGLGRIRSKFNNKAYDPKAIITANLTCKKPDQHFYPYLKQH 480
Db 421 RTFELSNLYTNVDDITLVPGTGLGRIRSKFNNKAYDPKAIITANLTCKKPDQHFYPYLKQH 480
QY 481 LPKRLHYANNRRRIEDIHLLYERHWHVARKPLDVYKPKSGKFFGQDGHGFDNKNVSMQTVF 540
Db 481 LPKRLHYANNRRRIEDIHLLYERHWHVARKPLDVYKPKSGKFFGQDGHGFDNKNVSMQTVF 540
QY 541 VGGPTEFKYTKVPPFENIELYNNVMDLLGLKPAPNNGTHGLNHLNTFRPTMPPEV 600
Db 541 VGGPTEFKYTKVPPFENIELYNNVMDLLGLKPAPNNGTHGLNHLNTFRPTMPPEV 600
QY 601 TRNYPGIMYLSQDFDLGCTCDKVEPKNKIDELNKLRLTKGSTFEERHLLYGRPAVLRYT 660
Db 601 TRNYPGIMYLSQDFDLGCTCDKVEPKNKIDELNKLRLTKGSTFEERHLLYGRPAVLRYT 660
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRYSPFSQNC 720
Db 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRYSPFSQNC 720
QY 721 AYKNDQMSYGFLEPPYLSLSSPEAKYDAFLVTNNVMPYPAFKRVWNTFORVLVKKYASER 780
Db 721 AYKNDQMSYGFLEPPYLSLSSPEAKYDAFLVTNNVMPYPAFKRVWNTFORVLVKKYASER 780
QY 781 NGVNVISGPIFDYDGLHDEKIKOYVGGSSIPVPTHYISITCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHDEKIKOYVGGSSIPVPTHYISITCLDFTQPADKCDGP 840
QY 841 LSVSSFLPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDFFRKTSRSYPE 900
Db 841 LSVSSFLPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDFFRKTSRSYPE 900
QY 901 ILTKYLYHYESEI 915
Db 901 ILTKYLYHYESEI 915
```

RESULT 4

US-08-346-455B-34
Sequence 34, Application US/08346455B
Patent No. 5731167

GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin

US-08-346-455B-34

Query Match 90.3%; Score 4533; DB 1; Length 829;
Best Local Similarity 99.9%; Pred No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 87 CHDFDELCLKTARGWECKTDCRCGEVRNEENACHCEDCLARGDCCTNYQVVCCKGESHWD 146
Db 1 CHDFDELCLKTARGWECKTDCRCGEVRNEENACHCEDCLARGDCCTNYQVVCCKGESHWD 60
QY 147 DCEIKAACCPAGFVRPPLIIFSVGDGFRASTMMKSKVMPNIEKLRSCGTHSPYMRPVY 206
Db 61 DCEIKAACCPAGFVRPPLIIFSVGDGFRASTMMKSKVMPNIEKLRSCGTHSPYMRPVY 120
QY 207 PKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGGOPLTATK 266
Db 121 PKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGGOPLTATK 180
QY 267 QGVKAGTFWSVVIPIHERRILTLRLWTLPLDHERPSVAFYSEQPDFSGHKYGFPGPEES 326
Db 181 QGVKAGTFWSVVIPIHERRILTLRLWTLPLDHERPSVAFYSEQPDFSGHKYGFPGPEES 240
QY 327 SYGSPFTPAKRPRKVPAPKRRROERPAPPKRRRKIRHMDHYAAETRODKMTPNLEIDK 386
Db 241 SYGSPFTPAKRPRKVPAPKRRROERPAPPKRRRKIRHMDHYAAETRODKMTPNLEIDK 300
QY 387 IVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNLYTNVDDITLVPGTLGRIR 446
Db 301 IVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNLYTNVDDITLVPGTLGRIR 360
QY 447 SKFSNNAYDPKAIITANLTCKKPDQHFYPYLKQHLPKRLHYANNRRRIEDIHLLYERHWHV 506
Db 361 SKFSNNAYDPKAIITANLTCKKPDQHFYPYLKQHLPKRLHYANNRRRIEDIHLLYERHWHV 420
QY 507 ARKPLDVYKPKSGKFFGQDGHGFDNKNVSMQTVFVGYGPTFKYTKVPPFENIELYNNVNC 566
|||||
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Db 421 ARKPLDVYKKPSGKCFQGDHGFNDKVNMSQTVFVGYGTEKYTKVPPENIELYNVMC 480
Qy 567 DLLGLKAPANNTHGSLNHLRTNFRPMPBEVTRPNYPGIMYLOSDFLGCTCDDKVE 626
Db 481 DLLGLKAPANNTHGSLNHLRTNFRPMPBEVTRPNYPGIMYLOSDDDLGCTCDDKVE 540
Qy 627 PKNKIDELNKLRLTKGSTERHLLYGRPAVLRYTRVDILYHTDFESGYSEIFLMLLWTSY 686
Db 541 PKNKIDELNKLRLTKGSTERHLLYGRPAVLRYTRVDILYHTDFESGYSEIFLMLLWTSY 600
Qy 687 TVSKQAEVSSVPDHLTSCVRPDVRSVPSFQSNCLAYKNDKQMSYGFLLPPLSSSSPEAKY 746
Db 601 TVSKQAEVSSVPDHLTSCVRPDVRSVPSFQSNCLAYKNDKQMSYGFLLPPLSSSSPEAKY 660
Qy 747 DAFVLTVMVMPYPAFKRVWNYFORVLVKKYASERNGVNVISGPIFYDYDGLDHTDEKIK 806
Db 661 DAFVLTVMVMPYPAFKRVWNYFORVLVKKYASERNGVNVISGPIFYDYDGLDHTDEKIK 720
Qy 807 QVVEGSSIPVPHYYSITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCSSEDESK 866
Db 721 QVVEGSSIPVPHYYSITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCSSEDESK 780
Qy 867 WVEELMKMHTARVDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYSEI 915
Db 781 WVEELMKMHTARVDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYSEI 829

RESULT 5
US-08-977-221-34
; Sequence 34, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 829

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Melanoma
; CELL LINE: A2058
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Putative protein
; OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-977-221-34

Query Match 90.3%; Score 4533; DB 3; Length 829;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 87 CHDFDELCLKTARGWECTKRCRGEVRNEENACHCEDECLARGDCCTNYQVCKGESHWVD 145
Db 1 CHDFDELCLKTARGWECTKRCRGEVRNEENACHCEDECLARGDCCTNYQVCKGESHWVD 60
Qy 147 DCCEIEKAAECPCAGFVRPPLIIFSVDFRASYMKKSKVMPNIEKLRSCGTHSPYMRPVY 206
Db 61 DCCEIEKAAECPCAGFVRPPLIIFSVDFRASYMKKSKVMPNIEKLRSCGTHSPYMRPVY 120
Qy 207 PTKTFPNLYLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGWGQPLWITATK 266
Db 121 PTKTFPNLYLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGWGQPLWITATK 180
Qy 267 QGVKAGTFEWSVWIPHERRILTLRWLTLPDHERPSYAFYSEQPDFSGHKYGFPGPEES 326
Db 181 QGVKAGTFEWSVWIPHERRILTLRWLTLPDHERPSYAFYSEQPDFSGHKYGFPGPEES 240
Qy 327 SYGSPFTPAKRPKRVKAPKRRQERPAPPKRRRKIRHMDHYAAETRODKMKNPLREIDK 386
Db 241 SYGSPFTPAKRPKRVKAPKRRQERPAPPKRRRKIRHMDHYAAETRODKMKNPLREIDK 300
Qy 387 IVGQMDGLKQLKLRRCNVNIFVGDHGMEDVTCDRTEFLSNLYTNVDDITLVPCTLGRIR 446
Db 301 IVGQMDGLKQLKLRRCNVNIFVGDHGMEDVTCDRTEFLSNLYTNVDDITLVPCTLGRIR 360
Qy 447 SKFSNNAKYDPKAIANLTCCKPDQHFKPYLKQHLPRLHYANNRRIEDTHLLVERWHV 506
Db 361 SKFSNNAKYDPKAIANLTCCKPDQHFKPYLKQHLPRLHYANNRRIEDTHLLVERWHV 420
Qy 507 ARKPLDVYKKPSGKCFQGDHGFNDKVNMSQTVFVGYGTEKYTKVPPENIELYNVMC 566
Db 421 ARKPLDVYKKPSGKCFQGDHGFNDKVNMSQTVFVGYGTEKYTKVPPENIELYNVMC 480
Qy 567 DLLGLKAPANNTHGSLNHLRTNFRPMPBEVTRPNYPGIMYLOSDFLGCTCDDKVE 626
Db 481 DLLGLKAPANNTHGSLNHLRTNFRPMPBEVTRPNYPGIMYLOSDDDLGCTCDDKVE 540
Qy 627 PKNKIDELNKLRLTKGSTERHLLYGRPAVLRYTRVDILYHTDFESGYSEIFLMLLWTSY 686
Db 541 PKNKIDELNKLRLTKGSTERHLLYGRPAVLRYTRVDILYHTDFESGYSEIFLMLLWTSY 600
Qy 687 TVSKQAEVSSVPDHLTSCVRPDVRSVPSFQSNCLAYKNDKQMSYGFLLPPLSSSSPEAKY 746
Db 601 TVSKQAEVSSVPDHLTSCVRPDVRSVPSFQSNCLAYKNDKQMSYGFLLPPLSSSSPEAKY 660
Qy 747 DAFVLTVMVMPYPAFKRVWNYFORVLVKKYASERNGVNVISGPIFYDYDGLDHTDEKIK 806

Db 661 DAFLVTNMVPMYPAKRWNYFQRLVKYASRNGVNVISGPIFDYDGLHDTEDKIK 720
QY 807 QYVEGSSIPVTHYISITCLDFTQADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 866
Db 721 QYVEGSSIPVTHYISITCLDFTQADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 780
QY 867 WVEELMKMHTARVRDIEHLTSLDFFRKTSTRSYPEILTLKTYLHTYSEI 915
Db 781 WVEELMKMHTARVRDIEHLTSLDFFRKTSTRSYPEILTLKTYLHTYSEI 829

RESULT 6
PCT-US95-06613-34
; Sequence 34, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 829
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Melanoma
; CELL LINE: A2058
; ORGANELLE:

; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Putative protein
; OTHER INFORMATION: sequence of A2058 Autotaxin
PCT-US95-06613-34

Query Match 90.3%; Score 4533; DB 5; Length 829;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 CHDFELCLKTARGWECTKDRCEVNEENACHCSBDCLARGDCCTNYQVCKGESHWD 146
Db 1 CHDFELCLKTARGWECTKDRCEVNEENACHCSBDCLARGDCCTNYQVCKGESHWD 60

QY 147 DCEELKAAECAGFVRPPLIIFSDGFRASYMKGSKVMPNIEKLRSCGTHSPYMRPY 206
Db 61 DCEELKAAECAGFVRPPLIIFSDGFRASYMKGSKVMPNIEKLRSCGTHSPYMRPY 120

QY 207 PKTTPNLYTLATGLYPESHGIVGNSMDPVDFATFHLRGKFNHRMGGQPLWITATK 266
Db 121 PKTTPNLYTLATGLYPESHGIVGNSMDPVDFATFHLRGKFNHRMGGQPLWITATK 180

QY 267 QGVKAGTFEWSVIPHERRILTLRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEES 326
Db 181 QGVKAGTFEWSVIPHERRILTLRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEES 240

QY 327 SYGSPFTPAKRPRKVPAPRRQRPVAPPKRRRKTHRMDHYAAETRODKMNPRLREIDK 386
Db 241 SYGSPFTPAKRPRKVPAPRRQRPVAPPKRRRKTHRMDHYAAETRODKMNPRLREIDK 300

QY 387 IVGQLMDGLKQLRRCVNVIFVGDHGMEDVTCDRTEFLSNVLTNVDDITLVPGTIGLR 446
Db 301 IVGQLMDGLKQLRRCVNVIFVGDHGMEDVTCDRTEFLSNVLTNVDDITLVPGTIGLR 360

QY 447 SKFSNNAKYDPKAIITANLTCCKPQDQHFYKQHLKRLHYANNRRIEDIHLIVERHWV 506
Db 361 SKFSNNAKYDPKAIITANLTCCKPQDQHFYKQHLKRLHYANNRRIEDIHLIVERHWV 420

QY 507 ARKPLDVKYKSGKCFQGDHGFNDKVNMSQTVFVGYGTFKYKTKVPFENIELYNVVC 566
Db 421 ARKPLDVKYKSGKCFQGDHGFNDKVNMSQTVFVGYGTFKYKTKVPFENIELYNVVC 480

QY 567 DILGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMYLOSDFLCTCDKVE 626
Db 481 DILGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMYLOSDFLCTCDKVE 540

QY 627 PKNKLDLNLKRLHTKGSTERRHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSY 686
Db 541 PKNKLDLNLKRLHTKGSTERRHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSY 600

QY 687 TVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSYGFLLPPYLSSEPEAKY 746
Db 601 TVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSYGFLLPPYLSSEPEAKY 660

QY 747 DAFLVTNMVPMYPAKRWNYFQRLVKYASRNGVNVISGPIFDYDGLHDTEDKIK 806
Db 661 DAFLVTNMVPMYPAKRWNYFQRLVKYASRNGVNVISGPIFDYDGLHDTEDKIK 720

QY 807 QYVEGSSIPVTHYISITCLDFTQADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 866
Db 721 QYVEGSSIPVTHYISITCLDFTQADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 780

QY 867 WVEELMKMHTARVRDIEHLTSLDFFRKTSTRSYPEILTLKTYLHTYSEI 915
Db 781 WVEELMKMHTARVRDIEHLTSLDFFRKTSTRSYPEILTLKTYLHTYSEI 829

RESULT 7
US-08-346-455B-67
; Sequence 67, Application US/08346455B

Patent No. 5731167
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-346-455B-67

Query Match 88.0%; Score 4418; DB 1; Length 861;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;

Qy 1 MARRSFSQCIISLFTFVAVGVICLGTFAHRIKRAEGWEGPPTVLSDSPWNTISGSCK 60
Db 1 MARRSFSQCIISLFTFVAVGVICLGTFAHRIKRAEGWEGPPTVLSDSPWNTISGSCK 60
Qy 61 GRCELOEAGPPDCRDLNCKSYTSCCHDFDELCLKTARGWECTKDRCEVNEENACHC 120
Db 61 GRCELOEAGPPDCRDLNCKSYTSCCHDFDELCLKTARGWECTKDRCEVNEENACHC 120
Qy 121 SEDCLARGDCTCTNYOVCKGESHWWDDCEETKAAECAPAGFVRPPLIIFSVDFGRASYNK 180
Db 121 SEDCLARGDCTCTNYOVCKGESHWWDDCEETKAAECAPAGFVRPPLIIFSVDFGRASYNK 180
Qy 181 KGSVMNPNIKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMIDPVFDA 240

Db 181 KGSVMNPNIKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMIDPVFDA 240
Qy 241 TFHLRGREKFNHRWGGOPWITATKQGVKAGTFWSVVI---PHERRILTLRWLTLP 296
Db 241 TFHLRGREKFNHRWGGOPWITATKQGVKAGTFWSVVI---PHERRILTLRWLTLP 296
Qy 297 DHER-----PSVYAFYSEQPDFSGHKYGFPGPESSYSGSPFTPAKRKRKVAPKRQRPV 352
Db 297 DHERLRSMPSILSNL-----ISLDTNMPFGE----- 323
Qy 353 APPKRRRKIHRMDHYAAETQDKWTNPLREIDKIVGQMDGLKQLKLRRCVNVIFVGDH 412
Db 324 -----MTNPLREIDKIVGQMDGLKQLKLRRCVNVIFVGDH 359
Qy 413 GMEDVTCDRTEFLSNLYTNVDDITLVPGTGLGRSKFSNNAKYDPKATIANLTCKKPDQ 472
Db 360 GMEDVTCDRTEFLSNLYTNVDDITLVPGTGLG-IRSKFSNNAKYDPKATIANLTCKKPDQ 418
Qy 473 FKPYLKQHLKRLHYANNRRIEDIHLVERRHWVARKPLDVKYKPSGKCFQGDHGFDMK 532
Db 419 FKPYLKQHLKRLHYANNRRIEDIHLVERRHWVARKPLDVKYKPSGKCFQGDHGFDMK 478
Qy 533 VNSMOTVFGYGYGPTFKYTKVPPFENIELYNMCDLLGLKLPAPNNGTHGSLNHLRTN 592
Db 479 VNSMOTVFGYGYGPTFKYTKVPPFENIELYNMCDLLGLKLPAPNNGTHGSLNHLRTN 538
Qy 593 RPTMPEEVTFRPNYPCIMYLSQDFDLGCTCDKVPKPKLDELNKLRLHTKGSTERHLLYG 652
Db 539 RPTMPEEVTFRPNYPCIMYLSQDFDLGCTCDKVPKPKLDELNKLRLHTKGSTERHLLYG 598
Qy 653 RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTSVSKAEVSSVDPDLTSCVRPDRVS 712
Db 599 RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTSVSKAEVSSVDPDLTSCVRPDRVS 658
Qy 713 PSFQNCCLAYKNDKQMSYGLFPYLSLSSPEAKYDAFLVTNMVPMYPAKRVWNYFORVL 772
Db 659 PSFQNCCLAYKNDKQMSYGLFPYLSLSSPEAKYDAFLVTNMVPMYPAKRVWNYFORVL 718
Qy 773 VKYASRNGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYISITSLDFTQ 832
Db 719 VKYASRNGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYISITSLDFTQ 778
Qy 833 PADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDIEHLTSLDFFR 892
Db 779 PADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDIEHLTSLDFFR 838
Qy 893 KTSRSEPEILTLKTYLHTYSEI 915
Db 839 KTSRSEPEILTLKTYLHTYSEI 861

RESULT 8
US-08-977-221-67
Sequence 67, Application US/08977221
Patent No. 6084069
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-977-221-67

Query Match 88.0%; Score 4418; DB 3; Length 861;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;

QY 1 MARRSSQSCQIISLFTFANGVSTCLGTAHRIKRAEWEGPPTVLSDSPWNTISGCK 60
DB 1 MARRSSQSCQIISLFTFANGVSTCLGTAHRIKRAEWEGPPTVLSDSPWNTISGCK 60
QY 61 GRCFELQAGPPDCRCNLCCKSVTSCCHDFDELCLKTARGNECKDRGGEVRNEENACHC 120
DB 61 GRCFELQAGPPDCRCNLCCKSVTSCCHDFDELCLKTARGNECKDRGGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVYCKGESHVDDDCERIKAAECFAGFVRPPLIIFSVDFGFRASYMK 180
DB 121 SEDCLARGDCCTNYQVYCKGESHVDDDCERIKAAECFAGFVRPPLIIFSVDFGFRASYMK 180
QY 181 KGSVMNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMVDPVDA 240
DB 181 KGSVMNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMVDPVDA 240
QY 241 TFLHGRGKFNHRWGGGLOPLWITATKGVKAGTFWVVI---PHERRILTLRLWTLPL 296
DB 241 TFLHGRGKFNHRWGGGLOPLWITATKGVKAGTFWVVI---PHERRILTLRLWTLPL 296
QY 297 DHER-----PSVIAYFSEQDFSGHKYGFPGPESSYSGPFTPAKRKRKVPKRQRPV 352
DB 297 DHERLRSMPSTLSNL-----ISLDTNMPGPE----- 323
QY 353 APPKRRRKHTRMDHYAETFRQDKMTNPLREIDKIVGOLMDGLKQLKLRRCVNVIFVGDH 412
DB 324 -----MTNPLREIDKIVGOLMDGLKQLKLRRCVNVIFVGDH 359
QY 413 GMEDVTCDRTEFLSNLTNVDITLVPGTGLGRISKFSNNAKYDPAKAIANTCKKPDQH 472
DB 360 GMEDVTCDRTEFLSNLTNVDITLVPGTGL-IRSKFSNNAKYDPAKAIANTCKKPDQH 418

QY 473 FKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFDMK 532
DB 419 FKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFDMK 478
QY 533 VNSMOTVFGVGYGPTFKYKTKVPPFENIELYNVMDLLGLKPPANNCTHGLSLHLLRTNTF 592
DB 479 VNSMOTVFGVGYGPTFKYKTKVPPFENIELYNVMDLLGLKPPANNCTHGLSLHLLRTNTF 538
QY 593 RPTMPEEVTNPYPGIMYLOSDFDLGCTCDDKVEPKNKLDLNLKRLHTKGTSTEEERHLLYG 652
DB 539 RPTMPEEVTNPYPGIMYLOSDFDLGCTCDDKVEPKNKLDLNLKRLHTKGTSTEEERHLLYG 598
QY 653 RPAVLYRTRIDYLYHTDFESGYSEIFLMLLWTSTYVSKQAEVSSVPDHLTSCVRPDVRS 712
DB 599 RPAVLYRTRIDYLYHTDFESGYSEIFLMPLWTSTYVSKQAEVSSVPDHLTSCVRPDVRS 658
QY 713 PSFSONCLAYKNDKQMSYGFLEPPYLSSSPSEAKYDAFLVTNMPVMPAPKRVNMYFQVRL 772
DB 659 PSFSONCLAYKNDKQMSYGFLEPPYLSSSPSEAKYDAFLVTNMPVMPAPKRVNMYFQVRL 718
QY 773 VKKYASERNGVNVISGPIDYDYGDLHDTEDKIKQYVEGSSIPVPHYYSITSCLDFTQ 832
DB 719 VKKYASERNGVNVISGPIDYDYGDLHDTEDKIKQYVEGSSIPVPHYYSITSCLDFTQ 778
QY 833 PADKCDGPLSVSFIPLPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFR 892
DB 779 PADKCDGPLSVSFIPLPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFR 838
QY 893 KTSRSYPEILTLKTYLHTYSEI 915
DB 839 KTSRSYPEILTLKTYLHTYSEI 861

RESULT 9
PCT-US95-06613-67
Sequence 67, Application PC/TUS9506613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434

; REFERENCE/DOCKET NUMBER: 2036-4149US2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 751-6849
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 67:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 861
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FEATURE:
 ; NAME/KEY: N-tera 2D1 ATX protein
 ; LOCATION:
 ; IDENTIFICATION METHOD:
 ; OTHER INFORMATION:
 PCT-US95-06613-67

Query Match 88.0%; Score 4418; DB 5; Length 861;
 Best Local Similarity 89.1%; Pred. No. 0;
 Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;
 QY 1 MARRSFSQSCIIISLFTFAVGSICLGTFAHRIKRAEGWEEGPTVLSDSPWNTNISGCK 60
 DB 1 MARRSFSQSCIIISLFTFAVGSICLGTFAHRIKRAEGWEEGPTVLSDSPWNTNISGCK 60
 QY 61 GRCFELQEAAGPDCRCNLCCKTSCHDFDELCLATARGWECTKDCGGEVRNEENACHC 120
 DB 61 GRCFELQEAAGPDCRCNLCCKTSCHDFDELCLATARGWECTKDCGGEVRNEENACHC 120
 QY 121 SEDCLARGDCCNYQVCKGESHWDDDEEIKAAECAPAGFVRPPLIFSVGDFRASVYM 180
 DB 121 SEDCLARGDCCNYQVCKGESHWDDDEEIKAAECAPAGFVRPPLIFSVGDFRASVYM 180
 QY 181 KSKVMPNIEKLRSCTHSPYRPPVPTKTFPNLYTLATGLYPESHGIVGNSMDPVFDA 240
 DB 181 KSKVMPNIEKLRSCTHSPYRPPVPTKTFPNLYTLATGLYPESHGIVGNSMDPVFDA 240
 QY 241 TPLHGREKFNHRWGGQPLWTATKQGVKAGTFEWSVVI---PHERRILTLRLWLTLP 296
 DB 241 TPLHGREKFNHRWGGQPLWTATKQGVKAGTFEWSVVI---PHERRILTLRLWLTLP 296
 QY 297 DHER---PSVYAFYSEQDFSGHKYGPFGPESSYSGSPFPAKRPKRKVAPKRRQRPV 352
 DB 297 DHERLRSMPILSNL-----ISLDTNMPGPE----- 323
 QY 353 APPKRRRKIHRMDHYAAETRODKWTNPLREIDKIVQLMDGLKQLKRCVNVIFVGDH 412
 DB 324 -----MTNPLREIDKIVQLMDGLKQLKRCVNVIFVGDH 359
 QY 413 GMEDVTCRTEFLSNVLTNVDITLVPGLTGRIRSKFSNNAKYDPAKIANLACKKPDQH 472
 DB 360 GMEDVTCRTEFLSNVLTNVDITLVPGLTGRIRSKFSNNAKYDPAKIANLACKKPDQH 418
 QY 473 FKPYLKQHLKPLKRLHYANNRRIEDHLLVRRHVARPLDYVKKPSGCKPFGQDHGFDNK 532
 DB 419 FKPYLKQHLKPLKRLHYANNRRIEDHLLVRRHVARPLDYVKKPSGCKPFGQDHGFDNK 478
 QY 533 VNSMOTVFVGYPGTPKYTKVPFFENIELYNVMDLGLKAPANNNGTHGSLNHLRTNTF 592
 DB 479 VNSMOTVFVGYPGTPKYTKVPFFENIELYNVMDLGLKAPANNNGTHGSLNHLRTNTF 538
 QY 593 RPTMPEEYTRPNYGMVYQSDFDLGCTCDDKVEPKNKLDLNLKRLHTKGTSTEEHLLYG 652
 DB 539 RPTMPEEYTRPNYGMVYQSDFDLGCTCDDKVEPKNKLDLNLKRLHTKGTSTEEHLLYG 598
 QY 653 RPAVLYRTYDILYHTDFESGSEIFLMLLTSTYTSKQAEVSSVPDHLTSCVRPDVRVS 712
 DB 599 RPAVLYRTYDILYHTDFESGSEIFLMLLTSTYTSKQAEVSSVPDHLTSCVRPDVRVS 658
 QY 713 PSFSONCLAYKNDKMSYGFLEPPYLSSSPEAKYDAFLVTNMPVMPYPAFKRVWNVTFQRLV 772

DB 659 PSFSONCLAYKNDKMSYGFLEPPYLSSSPEAKYDAFLVTNMPVMPYPAFKRVWNVTFQRLV 718
 QY 773 VKYASERNGVNIVSGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSLDFTQ 832
 DB 719 VKYASERNGVNIVSGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSLDFTQ 778
 QY 833 PADKCDGPLSVSSFTLPHRPDNEESCNSSEDESKVWEELMKMHTARVRDIEHLTSLDFFR 892
 DB 779 PADKCDGPLSVSSFTLPHRPDNEESCNSSEDESKVWEELMKMHTARVRDIEHLTSLDFFR 838
 QY 893 KTSRYPEILTLKTYLHTYSEI 915
 DB 839 KTSRYPEILTLKTYLHTYSEI 861
 RESULT 10
 US-08-346-455B-38
 ; Sequence 38, Application US/08346455B
 ; Patent No. 5731167
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT.
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/346,455B
 ; FILING DATE: 28-NOV-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06613
 ; FILING DATE: 24-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/249,182
 ; FILING DATE: 25-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/822,043
 ; FILING DATE: 17-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DOROTHY R. AUTH
 ; REGISTRATION NUMBER: 36,434
 ; REFERENCE/DOCKET NUMBER: 2036-4149PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 751-6849
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 38:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 979
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Human
 ; STRAIN:
 ; INDIVIDUAL ISOLATE:
 ; DEVELOPMENTAL STAGE:
 ; HAPLOTYPE:

TISSUE TYPE: Liver

CELL TYPE:

CELL LINE:

ORGANELLE:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: putative autotaxin

OTHER INFORMATION: protein sequence from human liver

US-08-346-455B-38

Query Match

Best Local Similarity 85.38; Score 4279; DB 1; Length 979;

Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;

QY 1 MARRSSFSQSCQIISLFTFAVGVSICLGTATRIKRAEGWEGPPVLSDSPWNTISGSK 60
DB 1 MARRSSFSQSCQIISLFTFAVGVSICLGTATRIKRAEGWEGPPVLSDSPWNTISGSK 60
QY 61 GRCFELQAGPPDCRCDNLKSYTSCCHDFDELCLKTARGWECTKDRGGEVRNEENACHC 120
DB 61 GRCFELQAGPPDCRCDNLKSYTSCCHDFDELCLKTARGWECTKDRGGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNTQVCKGESHVWDDCEIKAECAGFVRPPLIIFSVDFG--RASY 178
DB 121 SEDCLARGDCCTNTQVCKGESHVWDDCEIKAECAGFVRPPLIIFSVDFG--RASY 178
QY 179 MKGSKVMPNLEKLRSCGTHSPYMRPVYPTKFNLYTLATGLYPESHGIVGNSMYDPVF 238
DB 179 MKGSKVMPNLEKLRSCGTHSPYMRPVYPTKFNLYTLATGLYPESHGIVGNSMYDPVF 238
QY 239 DATFHLRGREKFNHRWGGQPLWTATKQGVKAGTFEWSVVI-----PHERILLITILRLT 294
DB 239 DATFHLRGREKFNHRWGGQPLWTATKQGES-----WNILLVCCHPRAELITILQWLT 294
QY 295 LPHERSVYAFYSEQDFGSKYKGPQGPBESSYSPPTPAKRKRKVAPKRQRVPAP 354
DB 295 LPHERSVYAFYSEQDFGSKYKGPQGPBESSYSPPTPAKRKRKVAPKRQRVPAP 354
QY 355 PKRRRKIRHRMDHYAAETRODKMTNPLREIDKIVCOLMDGLKOLKLRVNVVIFVGDHGM 414
DB 325 -----MTNPLREHKIVCOLMDGLKOLKLRVNVVIFVGDHGM 414
QY 415 EDVTCD--RTEFLSNLTNVDITLPGTLGRIRSKFSNNAKYDPKAIANTLCKKPDQH 472
DB 360 MDGRCHMYRTEFLSNLTNVDITLPGTLGRIRSKFSNNAKYDPKAIANTLCKKPDQH 419
QY 473 FKPYLKQHLKRLHYANNRRTEDHLLVERRHHVARKPLDYVKPSGKCFQGDHGFDMK 532
DB 420 FKPYLKQHLKRLHYANNRRTEDHLLVERRHHVARKPLDYVKPSGNAFSETTAFOFNK 479
QY 533 VNSMOTVFVGYPGTFKTKYKPPENTELYVMCDLLGKLPAPNNGTGLSNHLLRTNTF 592
DB 480 VNSMOTVFVGYPGTFKTKYKPPENTELYVMCDLLGKLPAPNNGTGLSNHLLRTNTF 539
QY 593 RPTMPEEVTREPNYIGIMYLOSDFDLCTCDKVEPKNKLDELNKLHKTGSTEERHLLYG 652
DB 540 RPTMPEEVTREPNYIGIMYLOSDFDLCTCDKVEPKNKLDELNKLHKTGSTEERHLLYG 599
QY 653 -RPAVLRYTRVDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRV 711
DB 600 DRPAVLRYTRVDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRV 659
QY 712 SPFSQNLAYKNQKQSYGLFPPLSSPEAKYDAFLVNMVPMYPAFRKRWNYFORV 771
DB 660 SPFSQNLAYKNQKQSYGLFPPLSSPEAKYDAFLVNMVPMYPAFRKRWNYFORV 719
QY 772 LVKYYASERNGVNIVSGPIFDYDGLDHTEDKIQYVEGSSIPVPTHYISITSCLDFT 831
DB 720 LVKYYASERNGVNIVSGPIFDYDGLDHTEDKIQYVEGSSIPVPTHYISITSCLDFT 779

QY 832 QPADKCDGPLSVSSSFLPHRPNESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDEFF 891
DB 780 QPADKCDGPLSVSSSFLPHRPNESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDEFF 839
QY 892 RKTSRSYPEILLTKTYLHTYSEI 915
DB 840 RKTSRSYPEILLTKTYLHTYSEI 863
RESULT 11
US-08-977-221-38
; Sequence 38, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE: Liver
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:

IDENTIFICATION METHOD:
; OTHER INFORMATION: putative autotaxin
; OTHER INFORMATION: protein sequence from human liver
US-08-977-221-38

Query Match	85.3%	Score 4279;	DB 3;	Length 979;
Best Local Similarity	87.1%	Pred. No. 0;		
Matches 805;	Conservative 13;	Mismatches 36;	Indels 70;	Gaps 8;

QY	1	MARRSFQSCQIISLTFVAVGVICLGFTHRIKRAEGWEEGPTVLSDSPWNTNISGSK	60
DB	1	MARRSFQSCQDLSLTFVAVGVNICLGFTHRIKRAEGWEEGPTVLSDSPWNTNISGSK	60
QY	61	GRCFELQERAGPPDCRDNLCCKSYTSCCHDFDELCLKTARWECTKDRGGEVRNEENACHC	120
DB	61	GRCFELQERAGPPDCRDNLCCKSYTSCCHDFDELCLKTARWECTKDRGGEVRNEENACHC	120
QY	121	SEDCLARGDCCNTYQVYCKGESHWDDCEEIKAAECPCAGFVRPPLIIFSVDGF--RAS	178
DB	121	SEDCLARGDCCNTYQVYCKGESHWDDCEEIKAAECPCAGFVRPPLIIFSVDGF--RAS	178
QY	179	MKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTPNNLYTLATGLYPESHGIVGNSMYDPVF	238
DB	179	MKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTPNNLYTLATGLYPESHGIVGNSMYDPVF	238
QY	239	DATFHLRGREKENHRWNGOPLMITAKOGVKAGTFWVVI----PHERRILTLRLWT	294
DB	239	DATFHLRGREKENHRWNGOPLMITAKOGES----WNILLVCCHPSRAEILTLQLWT	294
QY	295	LPDHERPSVYAFYSEQDPDSGHKYGFGPEESSYGSFPFPAKRPKRVAKRQERVPAP	354
DB	295	LPDHERPSVYAFYSEQDPDSGHKMFPGPE-----	324
QY	355	PKRRRKIRHMDHYAAETRODKMNTNPLREIDKIVGQIMDGLKOLKLRRCVNVIFVGDHGM	414
DB	325	-----MTNPLREMHKIVGQIMDGLKOLKLRRCVNVIFV----ET	359
QY	415	EDVTC--RTEFSLNLYTNVDDITLVPGLGRIRSKFSNNAKYDPAKAIANLTKCKPDQH	472
DB	360	MDGRCHMYRTEFSLNLYTNVDDITLVPGLGRIRSKFSNNAKYDPAKAIANLTKCKPDQH	419
QY	473	KPYLKLQHLPKRLHYANNRIEDIHLLVRRHWVARKPLDYKKPSGKFFQGDHGFENK	532
DB	420	KPYLKLQHLPKRLHYANNRIEDIHLLVRRHWVARKPLDYKKPSGNAPSRETTAFDNK	479
QY	533	VNSMOTVFYGYGPTFKYKTKVPFENIELYNVMDLLGLKLPAPNNGTHGSLNHLRLTNTF	592
DB	480	VNSMOTVFYGYGPTFKYKTKVPFENIELYNVMDLLGLKLPAPNNGTHGSLNHLRLTNTF	539
QY	593	RPTMPEEVRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHTKGSTEERHLLYG	652
DB	540	RPTMPEEVRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHTKGSTEERHLLYG	599
QY	653	RPVLYRTRYDILYHTDESGYSEIFLMLWTSTYVSKQAEVSSVPDHLTSCVRDPVRV	711
DB	600	DRPVLRYRTRYDILYHTDESGYSEIFLMLWTSTYVSKQAEVSSVPDHLTSCVRDPVRV	659
QY	712	SPFSQNCCLAYKNDKMSYGFPPYLSPPSSPEAKYDAFLVTNNMVPYPAFKRVNMYFQRV	771
DB	660	SPFSQNCCLAYKNDKMSYGFPPYLSPPSSPEAKYDAFLVTNNMVPYPAFKRVNMYFQRV	719
QY	772	LVKKYASERNGVNYSIGPIFYDYGDLHDETKIKOYVEGSSIPVPTHYYSIIITSLDFT	831
DB	720	LVKKYASERNGVNYSIGPIFYDYGDLHDETKIKOYVEGSSIPVPTHYYSIIITSLDFT	779
QY	832	QPADKCDGPLSVSSFTLPHRPNEESCNSDESKWVEELMKMHTARVRDIEHLTSLDFF	891
DB	780	QPADKCDGPLSVSSFTLPHRPNEESCNSDESKWVEELMKMHTARVRDIEHLTSLDFF	839
QY	892	RKTSRSPYELLTKYLYLHYESEI 915	
DB	840	RKTSRSPYELLTKYLYLHYESEI 863	

RESULT 12
PCT-US95-06613-38
; Sequence 38, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MORATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE: Liver
; CELL TYPE:
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: putative autotaxin
; OTHER INFORMATION: protein sequence from human liver
PCT-US95-06613-38

Query Match 85.3%; Score 4279; DB 5; Length 979;

Best Local Similarity 87.1%; Pred. No. 0;		Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;	
QY	1	MARRSSFSQSQIISLFTFAVGSICLGTAAHRIKRAEGWEEGPTVLSDSPWNTISGSK	60
Db	1	MARRSSFSQSQDISLFTFAVGVNICLGTAAHRIKRAEGWEEGPTVLSDSPWNTISGSK	60
QY	61	GRCFELQEAAGPPDCRCNLKSYTSCCHDFDELCLKTARGWECTKDRCGEVNRNEENACHC	120
Db	61	GRCFELQEAAGPPDCRCNLKSYTSCCHDFDELCLKTARGWECTKDRCGEVNRNEENACHC	120
QY	121	SECLARGDCCTNYQVCKGESHVWDDCEIKAECPAGFVRPPLIIFSVDFG--RASY	178
Db	121	SECLARGDCCTNYQVCKGESHVWDDCEIKAECLQ--VCSPSINHLRGLWLPWTYS	178
QY	179	MKGSGKMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLXPESHGIVGNSMYDPVF	238
Db	179	MKGSGKMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLXPESHGIVGNSMYDPVF	238
QY	239	DATFHLRGREKFNIRWGGQPLWTATKQGVKAGTFWVSVI-----PHERILLTLRLWT	294
Db	239	DATFHLRGREKFNIRWGGQPLWTATKQGES-----WNILLVCCHPGRAEITLLOWLT	294
QY	295	LPHERPSVAFYSEQPDFSGHKYGRGPRPSSYSGSPPTPAKRKRKYAPKRQERPVAP	354
Db	295	LPHERPSVAFYSEQPDFSGHKHMPGPE-----	324
QY	355	PKRRRRIRHMDHYAAETRODKMTNPLREIDKIVQLMDGLKQLKLRRCVNVIFVGDHGM	414
Db	325	-----MTNPLREMKIVQLMDGLKQLKLRRCVNVIFV--ET	359
QY	415	EDVTC--RTEFLSNLTNVDIDILVPGTLGRIRSKFSNNAKYDPKALIANLTKKPPQH	472
Db	360	MDGRCHMYRTEFLSNLTNVDIDILVPGTLGRIRSKFSNNAKYDPKALIANLTKKPPQH	419
QY	473	FKPYLQHLPKRLHYANNRRLEDIHLVERWHVARKPLDYVKKPSGCKEFGDGHGDNK	532
Db	420	FKPYLQHLPKRLHYANNRRLEDIHLVERWHVARKPLDYVKKPSGNAFSRETTAFDNK	479
QY	533	VNSMOTVFVGYPGTFKYKTKVPPFENIELYNVMDCLGLKAPNNGTHGSLNHLIRTNTF	592
Db	480	VNSMOTVFVGYPGTFKYKTKVPPFENIELYNVMDCLGLKAPNNGTHGSLNHLIRTNTF	539
QY	593	RPMPEEVRPNYPGIMYLOSDFDLCTDDKVPKKNLDELNKLRLHTKGSTEEHLLYG	652
Db	540	RPMPEEVRPNYPGIMYLOSDFDLCTDDKVPKKNLDELNKLRLHTKGSTEEHLLYG	599
QY	653	-RAVLRYTRDYDILYHTDFESGYSEIFLMLLWTSYVSKQAEVSSVPDHLTSCVRPDYRV	711
Db	600	DRFAVLRYTRDYDILYHTDFESGYSEIFLMLWTSYVSKQAEVSSVPDHLTSCVRPDYRV	659
QY	712	SPSFSQNLAYKNDKQMSYGLFPFPPYLSSSPEAKYDAPLVTNMVPMPYPAFKRVNMYFORV	771
Db	660	SPSFSQNLAYKNDKQMSYGLFPFPPYLSSSPEAKYDAPLVTNMVPMPYPAFKRVNMYFORV	719
QY	772	LVKYYASERNGVNIVSGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYISILTSCLDFT	831
Db	720	LVKYYASERNGVNIVSGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYISILTSCLDFT	779
QY	832	OPADKCDGPLSVSSFILPHRPDNEESCSNSEDKWKVEELMKMHTARVYDIEHLTSLDFF	891
Db	780	OPADKCDGPLSVSSFILPHRPDNEESCSNSEDKWKVEELMKMHTARVYDIEHLTSLDFF	839
QY	892	RKTSRSYPEILTLKTYLHTYESEI	915
Db	840	RKTSRSYPEILTLKTYLHTYESEI	863

RESULT 13
US-08-346-455B-36
; Sequence 36, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2036-4149PCT
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 788
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: teratocarcinoma
CELL LINE: N-tera 2D1
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: N-tera 2D1 putative
OTHER INFORMATION: ATX protein sequence
US-08-346-455B-36

Query Match 76.5%; Score 3842; DB 1; Length 788;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;

QY 76 CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVNRNEENACHCSDCLARGDCCTNTQ 135
Db 1 CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVNRNEENACHCSDCLARGDCCTNTQ 60

QY 136 VYCKGSHWVDDCEIEKAAECAPAGVRPLLIIFSVDFG--RASVMKKGSKVMPNIEKLR 193
Db 61 VYCKGSHWVDDCEIEKAAECQ--VDSFINHLRGWLPMTSYMKKGSKVMPNIEKLR 118
QY 194 SCGTHSPYMRPVYPTKTFPNLYLATGLYPESHGIVGNSMYDPVDFATFLRGREKFNHR 253
Db 119 SCGTHSPYMRPVYPTKTFPNLYLATGLYPESHGIVGNSMYDPVDFATFLRGREKFNHR 178
QY 254 WVGGOPLWITATKQGVKAGTFFWSVI----PHERILTLRLWLTLPDHERPSVYAFYSE 309
Db 179 WVGGOPLWITATKQGES----WNILLVCCHPRAEILTLQWLTLPDHERPSVYAFYSE 234
QY 310 QDFSGHKYGPFGPESSYGSFTPAKPKRVAPRRQRPVAPKRRKRLHRMDHYA 369
Db 235 QDFSGHKHMPGPE----- 249
QY 370 AETROKMTNPLREIDKIVQLMDGLKQLKRCVNVIFVGDHGMEDVTCD--RTEFLSN 427
Db 250 -----MPNPLREMHKIVQLMDGLKQLKRCVNVIFV--ETWDGRCHMYRTEFLSN 299
QY 428 YLTNVDDTLVPDGTIGRIRSKFSNNAKYPDKAIANLTCKKPDQHKPYLKQHLKRLHY 487
Db 300 YLTNVDDTLVPDGTIGRIRSKFSNNAKYPDKAIANLTCKKPDQHKPYLKQHLKRLHY 359
QY 488 ANNRIEDIHLVERHWVARKPLDYKKPSGCKPFGQDGHGFDKNVSMQTVFVGYPTE 547
Db 360 ANNRIEDIHLVERHWVARKPLDYKKPSGNAFSRETTAFDNKVNMQTVFVGYPTE 419
QY 548 KYTKVPPFENIELYNVMDLGLKAPNNGTHGSLNHLRLTNTFRPTMPEEVRTNYPG 607
Db 420 KYTKVPPFENIELYNVMDLGLKAPNNGTHGSLNHLRLTNTFRPTMPEEVRTNYPG 479
QY 608 IMYLOSDFDLGCTDDKVEPKNKLDELNKLRLHTKGTSTERHLLYG--RPAVLYRTRYDILY 666
Db 480 IMYLOSDFDLGCTDDKVEPKNKLDELNKLRLHTKGTSTERHLLYGDRPAVLYRTRYDILY 539
QY 667 HTDFESGYSEIFLMLLTWTSYTSKQAEVSSVPDHLTSCVRPDVVRVSPSONCLAYKNDK 726
Db 540 HTDFESGYSEIFLMLLTWTSYTSKQAEVSSVPDHLTSCVRPDVVRVSPSONCLAYKNDK 599
QY 727 QMSYGFLEPPYLSSPPEAKYDAFLTNMVMYPAKRVWNYFORVLVKKYASBRGNVNI 786
Db 600 QMSYGLGLPPYLSSPPEAKYDAFLTNMVMYPAKRVWNYFORVLVKKYASBRGNVNI 659
QY 787 SGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSF 846
Db 660 SGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSF 719
QY 847 ILPHRPDNEESCNSSEDESKWYEELMKMTARVDRDIEHLTSLDFFRKTSSYPEILTLKT 906
Db 720 ILPHRPDNEESCNSSEDESKWYEELMKMTARVDRDIEHLTSLDFFRKTSSYPEILTLKT 779
QY 907 YLHYEYSEI 915
Db 780 YLHYEYSEI 788

RESULT 14
US-08-977-221-36
; Sequence 36, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK

COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 788
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: teratocarcinoma
CELL TYPE: N-tera 2d1
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: N-tera 2d1 putative
OTHER INFORMATION: ATX protein sequence
US-08-977-221-36

Query Match 76.5%; Score 3842; DB 3; Length 788;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;

QY 76 CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCEVNRNEENACHCEDCLARGDCCTNYQ 135
Db 1 CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCEVNRNEENACHCEDCLARGDCCTNYQ 60
QY 136 VYCKGSHWVDDCEIEKAAECAPAGVRPLLIIFSVDFG--RASVMKKGSKVMPNIEKLR 193
Db 61 VYCKGSHWVDDCEIEKAAECQ--VDSFINHLRGWLPMTSYMKKGSKVMPNIEKLR 118
QY 194 SCGTHSPYMRPVYPTKTFPNLYLATGLYPESHGIVGNSMYDPVDFATFLRGREKFNHR 253
Db 119 SCGTHSPYMRPVYPTKTFPNLYLATGLYPESHGIVGNSMYDPVDFATFLRGREKFNHR 178
QY 254 WVGGOPLWITATKQGVKAGTFFWSVI----PHERILTLRLWLTLPDHERPSVYAFYSE 309
Db 179 WVGGOPLWITATKQGES----WNILLVCCHPRAEILTLQWLTLPDHERPSVYAFYSE 234

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QY 310 QPDFSGHKYGFCEPSESSYGSPFTPAKRPKRVKAPKRRQRPVAPPKRRKRIHRMDHYA 369
Db 235 QPDFSGHKHMPFGE-----249
QY 370 AETRODKMTNPLREIDKIVGQMDGLKQLKLRRCVNVIVFGDHGMEDVTC--RTEFLSN 427
Db 250 -----MPNPLREMHKIVQMDGLKQLKLRRCVNVIVF---ETMDGRCHMYRTEFLSN 299
QY 428 YLNVDDITLVPGTGLRIRSKFSNNAKYDPKAIITANITCKPDQHFKPYLKQHLPKRLHY 487
Db 300 YLNVDDITLVPGTGLRIRSKFSNNAKYDPKAIITANITCKPDQHFKPYLKQHLPKRLHY 359
QY 488 ANNRRIEDIHLLVERRHVARKPLDVYKKGSGCKFFQGDHGFDNKVNMQTVFVGYGTF 547
Db 360 ANNRRIEDIHLLVERRHVARKPLDVYKKGSGCKFFQGDHGFDNKVNMQTVFVGYGTF 419
QY 548 KYTKVPPFENIELYNMCDLGLKPAKPNNGTGHSLNHLRTNTFRPTMPEVTRPNYPG 607
Db 420 KYTKVPPFENIELYNMCDLGLKPAKPNNGTGHSLNHLRTNTFRPTMPEVTRPNYPG 479
QY 608 IMVLSDFDLGCTCDDKVEPKNLDELKRLHTKGSTEEHLLYG-RPAVLYRTRYDILY 666
Db 480 IMVLSDFDLGCTCDDKVEPKNLDELKRLHTKGSTEEHLLYGDRPAVLYRTRYDILY 539
QY 667 HTDFESGYSEIFLMLTSTVSKQAEVSSVDPDLTSCVRPDVRSVPSFQNCCLAYKNDK 726
Db 540 HTDFESGYSEIFLMLTSTVSKQAEVSSVDPDLTSCVRPDVRSVPSFQNCCLAYKNDK 599
QY 727 QMSYGFLLPPLSSSPKAYDAFLVTNVMYPAPKRVNMYFORVLVKKYASERNGVNI 786
Db 600 QMSYGFLLPPLSSSPKAYDAFLVTNVMYPAPKRVNMYFORVLVKKYASERNGVNI 659
QY 787 SGPIFYDYDGLHDTEDKIQYVSGSSIPVPTHYYSITSCLDFTQPADKCDGPLSVSSF 846
Db 660 SGPIFYDYDGLHDTEDKIQYVSGSSIPVPTHYYSITSCLDFTQPADKCDGPLSVSSF 719
QY 847 ILPHRPNEESCNSDESKWVEELMHMTARVDRDIEHLTSLDFRKTYSRYPEILTLTK 906
Db 720 ILPHRPNEESCNSDESKWVEELMHMTARVDRDIEHLTSLDFRKTYSRYPEILTLTK 779
QY 907 YLTYESEI 915
Db 780 YLTYESEI 788

RESULT 15
PCT-US95-06613-36
; Sequence 36, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-41490S2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: teratocarcinoma
; CELL LINE: N-tera 2D1
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: N-tera 2D1 putative
; OTHER INFORMATION: ATX protein sequence
;
PCT-US95-06613-36
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Query Match 76.5%; Score 3842; DB 5; Length 788;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;

QY 76 CDNLCKSYTSCCHDPELCLKTARGWECKTRCGRGEVRNEENACHCEDCLARGDCCTNTYQ 135
Db 1 CDNLCKSYTSCCHDPELCLKTARGWECKTRCGRGEVRNEENACHCEDCLARGDCCTNTYQ 60
QY 136 VYCKGESHVWDDCEIKAACPAAGFVRPPLIIFSVDF--RASVYMKGSKVMPNIEKLR 193
Db 61 VYCKGESHVWDDCEIKAACPAAGFVRPPLIIFSVDF--RASVYMKGSKVMPNIEKLR 118
QY 194 SCGTHSPYMRPVYPTKTPNLTATGLYPESHGIVGNSMDVDFVDFATFLRGREKFNHR 253
Db 119 SCGTHSPYMRPVYPTKTPNLTATGLYPESHGIVGNSMDVDFVDFATFLRGREKFNHR 178
QY 254 WNGGQPLWITATKQGVKAGTFFWSVI----PHERRILILRWLTLPDHERPSVYAFYE 309
Db 179 WNGGQPLWITATKQGVKAGTFFWSVI----PHERRILILRWLTLPDHERPSVYAFYE 234
QY 310 QPDFSGHKYGFCEPSESSYGSPFTPAKRPKRVKAPKRRQRPVAPPKRRKRIHRMDHYA 369
Db 235 QPDFSGHKHMPFGE-----249
QY 370 AETRODKMTNPLREIDKIVGQMDGLKQLKLRRCVNVIVFGDHGMEDVTC--RTEFLSN 427
Db 250 -----MPNPLREMHKIVQMDGLKQLKLRRCVNVIVF---ETMDGRCHMYRTEFLSN 299
QY 428 YLNVDDITLVPGTGLRIRSKFSNNAKYDPKAIITANITCKPDQHFKPYLKQHLPKRLHY 487
Db 300 YLNVDDITLVPGTGLRIRSKFSNNAKYDPKAIITANITCKPDQHFKPYLKQHLPKRLHY 359
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Db	300	YLTNVDDITLVPCTLGRIRSKFSNNAKYDPKALIANLTCCKKPDQHFKPYLKQHLPKRLHY	359
Qy	488	ANNRIEDIHLLVERWHVARKPLDYIKKPSGKCFQGDHGFNDKNYSMQTVFVGIGPTF	547
Db	360	ANNRIEDIHLLVERWHVARKPLDYIKKPSGNAFSRETTAFDNKNYSMQTVFVGIGPTF	419
Qy	548	KYKTKVPPPENIELXNVMCDLLGLKFPAPNGTHGSLNHLRLTNTFRPTMPEEVTTRPNYPG	607
Db	420	KYKTKVPPPENIELXNVMCDLLGLKFPAPNGTHGSLNHLRLTNTFRPTMPEEVTTRPNYPG	479
Qy	608	IMYLOSDFDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYG-RPAVLYRTRYDILY	666
Db	480	IMYLOSDFDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYGDRPAVLYRTRYDILY	539
Qy	667	HTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRSVSPSQNCLAYKNDK	726
Db	540	HTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRSVSPSQNCLAYKNDK	599
Qy	727	QMSYGFLEPPYLSSSPEAKYDAFLVTNMYPMYPAFKRVWNYFORVLVKKYASERNGVNI	786
Db	600	QMSYGFLEPPYLSSSPEAKYDAFLVTNMYPMYPAFKRVWNYFORVLVKKYASERNGVNI	659
Qy	787	SGPIFDYDYGDLHDEDKIKQYVEGSSIPVPTHYYSIITSCLDFTOPADKCDGPLSVSSF	846
Db	660	SGPIFDYDYGDLHDEDKIKQYVEGSSIPVPTHYYSIITSCLDFTOPADKCDGPLSVSSF	719
Qy	847	ILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFFRKTSRYP EILT LKT	906
Db	720	ILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFFRKTSRYP EILT LKT	779
Qy	907	YLHTYESEI 915	
Db	780	YLHTYESEI 788	

Search completed: July 19, 2001, 14:45:26
Job time: 179 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:26 ; Search time 20.45 Seconds
(without alignments)
12.806 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213

Perfect score: 76

Sequence: 1 YMRPVPTKTFPN 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	788	1 US-08-346-455B-36	Sequence 36, Appl
2	76	100.0	788	3 US-08-977-221-36	Sequence 36, Appl
3	76	100.0	788	5 PCT-US95-06613-36	Sequence 36, Appl
4	76	100.0	829	1 US-08-346-455B-34	Sequence 34, Appl
5	76	100.0	829	3 US-08-977-221-34	Sequence 34, Appl
6	76	100.0	829	5 PCT-US95-06613-34	Sequence 34, Appl
7	76	100.0	915	1 US-08-346-455B-69	Sequence 69, Appl
8	76	100.0	915	3 US-08-977-221-69	Sequence 69, Appl
9	76	100.0	915	5 PCT-US95-06613-69	Sequence 69, Appl
10	76	100.0	979	1 US-08-346-455B-38	Sequence 38, Appl
11	76	100.0	979	3 US-08-977-221-38	Sequence 38, Appl
12	76	100.0	979	5 PCT-US95-06613-38	Sequence 38, Appl
13	71	93.4	861	1 US-08-346-455B-67	Sequence 67, Appl
14	71	93.4	861	3 US-08-977-221-67	Sequence 67, Appl
15	71	93.4	861	5 PCT-US95-06613-67	Sequence 67, Appl
16	69	90.8	873	3 US-09-187-331-6	Sequence 6, Appl1
17	69	90.8	873	5 US-08-392-946-1	Sequence 1, Appl1
18	69	90.8	925	2 US-08-504-169-1	Sequence 1, Appl1
19	69	90.8	925	5 PCT-US94-14893-1	Sequence 1, Appl1
20	40	52.6	203	2 US-08-684-024-8	Sequence 8, Appl1
21	40	52.6	203	3 US-09-145-868-8	Sequence 8, Appl1
22	40	52.6	205	2 US-08-684-024-1	Sequence 1, Appl1
23	40	52.6	205	2 US-08-684-024-6	Sequence 6, Appl1
24	40	52.6	205	2 US-08-684-024-7	Sequence 7, Appl1
25	40	52.6	205	3 US-09-145-868-1	Sequence 1, Appl1
26	40	52.6	205	3 US-09-145-868-6	Sequence 6, Appl1
27	40	52.6	205	3 US-09-145-868-7	Sequence 7, Appl1

28	38	50.0	438	3	US-09-187-331-2	Sequence 2, Appl1
29	37	48.7	49	1	US-07-865-166A-6	Sequence 6, Appl1
30	37	48.7	254	2	US-08-207-481-20	Sequence 20, Appl1
31	37	48.7	254	5	PCT-US95-02689-20	Sequence 20, Appl1
32	37	48.7	264	2	US-08-484-905-120	Sequence 120, Appl1
33	37	48.7	264	3	US-08-481-985B-120	Sequence 120, Appl1
34	37	48.7	264	4	US-08-370-476-120	Sequence 120, Appl1
35	37	48.7	436	1	US-08-080-255-8	Sequence 8, Appl1
36	37	48.7	436	4	US-08-465-713-8	Sequence 8, Appl1
37	37	48.7	436	5	PCT-US93-05857-8	Sequence 8, Appl1
38	37	48.7	3969	4	US-08-061-376-5	Sequence 5, Appl1
39	36	47.4	309	3	US-08-989-644-20	Sequence 20, Appl1
40	36	47.4	309	4	US-08-444-189-20	Sequence 20, Appl1
41	36	47.4	359	2	US-08-560-398-10	Sequence 10, Appl1
42	36	47.4	516	4	US-09-201-641-6	Sequence 6, Appl1
43	36	47.4	707	1	US-08-528-122-18	Sequence 18, Appl1
44	36	47.4	707	5	PCT-US95-11720-18	Sequence 18, Appl1
45	36	47.4	750	1	US-08-325-553-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-346-455B-36
; Sequence 36, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein

;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE: Human
;; ORGANISM: Human
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE: teratocarcinoma
;; CELL LINE: N-tera 2D1
;; ORGANELLE:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: N-tera 2D1 putative
;; OTHER INFORMATION: ATX protein sequence
US-08-346-455B-36

Query Match 100.0%; Score 76; DB 1; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 126 YMRPVYPTKTFPN 138

RESULT 2
PCT-US95-06613-36
; Sequence 36, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA: 08/249,182
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 36:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 788
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Human
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE: teratocarcinoma
;; CELL LINE: N-tera 2D1
;; ORGANELLE:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: N-tera 2D1 putative
;; OTHER INFORMATION: ATX protein sequence
US-08-977-221-36
Query Match 100.0%; Score 76; DB 3; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YMRPVYPTKTFPN 13
Db 126 YMRPVYPTKTFPN 138
RESULT 3
PCT-US95-06613-36
; Sequence 36, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH

REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 788
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: teratocarcinoma
CELL LINE: N-tera 2D1
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: N-tera 2D1 putative
OTHER INFORMATION: ATX protein sequence
PCT-US95-06613-36

Query Match 100.0%; Score 76; DB 5; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13

Db 126 YMRPVYPTKTFPN 138

RESULT 4
US-08-346-455B-34
; Sequence 34, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346.455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182

FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA: 07/822,043
APPLICATION NUMBER:
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-346-455B-34

Query Match 100.0%; Score 76; DB 1; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13

Db 115 YMRPVYPTKTFPN 127

RESULT 5
US-08-977-221-34
; Sequence 34, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-41490S3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-977-221-34

Query Match 100.0%; Score 76; DB 3; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 115 YMRPVYPTKTFPN 127

RESULT 6
PCT-US95-06613-34
Sequence 34, Application PC/TUS9506613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-41490S2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: Melanoma
CELL TYPE: A2058
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
PCT-US95-06613-34
Query Match 100.0%; Score 76; DB 5; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YMRPVYPTKTFPN 13
Db 115 YMRPVYPTKTFPN 127
RESULT 7
US-08-346-455B-69
Sequence 69, Application US/08346455B
Patent No. 5731167
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE

```

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-41490S3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 915
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: No
FEATURE:
NAME/KEY: A2058 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-977-221-69

```

Query Match 100.0%; Score 76; DB 3; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels

```

9
PCT-US95-06613-69
; Sequence 69, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRÄCKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIEFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
PCT-US95-06613-69

Query Match 100.0%; Score 76; DB 5; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||

Db 201 YMRPVYPTKTFPN 213

RESULT 10
US-08-346-455B-38
; Sequence 38, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT...
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613

; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE: Liver
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: putative autotoxin
; OTHER INFORMATION: protein sequence from human liver
US-08-346-455B-38

Query Match 100.0%; Score 76; DB 1; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||

Db 201 YMRPVYPTKTFPN 213

RESULT 11
US-08-977-221-38
; Sequence 38, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1

```

RESULT 12
PCT-US95-06613-38
; Sequence 38, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE.;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CAN
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.

```

RESULT 13
US-08-346-455B-67
; Sequence 67: Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: U.S.A.
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/346,455B
;; FILING DATE: 28-NOV-1994
;; CLASSIFICATION: 530
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/06613
;; FILING DATE: 24-MAY-1995
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/249,182
;; FILING DATE: 25-MAY-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/822,043
;; FILING DATE: 17-JAN-1992
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DOROTHY R. AUTH
;; REGISTRATION NUMBER: 36,434
;; REFERENCE/DOCKET NUMBER: 2026-4149PCT
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 751-6849
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 861
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: N-tera 2D1 ATX protein
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;;
;; US-08-346-455B-67

Query Match 93.4%; Score 71; DB 1; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 201 HMRPVYPTKTFPN 213

RESULT 14
US-08-977-221-67
PCT-08-977-221-67
Sequence 67, Application US/08977221
Patent No. 6084069
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK

;; COUNTRY: U.S.A.
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/977,221
;; FILING DATE:
;; CLASSIFICATION:
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/346,455
;; FILING DATE: 28-NOV-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/249,182
;; FILING DATE: 25-MAY-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/822,043
;; FILING DATE: 17-JAN-1992
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DOROTHY R. AUTH
;; REGISTRATION NUMBER: 36,434
;; REFERENCE/DOCKET NUMBER: 2026-4149US3
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 751-6849
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 861
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: N-tera 2D1 ATX protein
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;;
;; US-08-977-221-67

Query Match 93.4%; Score 71; DB 3; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 201 HMRPVYPTKTFPN 213

RESULT 15
PCT-US95-06613-67
Sequence 67, Application PC/TUS9506613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06613-67

Query Match 93.4%; Score 71; DB 5; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 201 HMRPVYPTKTFPN 213

Search completed: July 19, 2001, 14:45:27
Job time: 180 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:43:22 ; Search time 25.97 Seconds
(without alignments)
2683.855 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSFQSCQIISLFTFAV.....RSYPEILTKLYLHTYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5019	100.0	915	1 A55144	autotaxin precursor
2	4306	85.8	885	1 A55453	plasma cell membra
3	2084	41.5	875	1 A57080	cell surface antig
4	1955.5	39.0	925	1 A39216	plasma cell membra
5	1899.5	37.8	905	1 A27410	plasma cell membra
6	646.5	12.9	457	2 T09932	nucleotide pyropho
7	612	12.2	496	2 T09931	nucleotide pyropho
8	611.5	12.2	479	2 T03293	nucleotide pyropho
9	610	12.2	829	2 T19494	hypothetical prote
10	609	12.1	461	2 T09933	nucleotide pyropho
11	539.5	10.7	485	2 T40657	probable phosphodi
12	522	10.4	429	2 T33724	hypothetical prote
13	461	9.2	433	2 B82537	phosphodiesterase-
14	456.5	9.1	674	2 T19495	hypothetical prote
15	456	9.1	300	2 A41179	protein kinase Pc-
16	410	8.2	743	2 S19437	hypothetical prote
17	335.5	6.7	493	2 S50443	hypothetical prote
18	297.5	5.9	614	2 T03973	hypothetical prote
19	241.5	4.8	133	2 T09934	hypothetical prote
20	238	4.7	96	2 A25274	phosphodiesterase
21	238	4.7	433	2 T16795	hypothetical prote
22	163	3.2	360	2 T20867	hypothetical prote
23	146.5	2.9	329	1 NCBYN1	nuclease NUC1 (EC
24	145.5	2.9	465	2 T34936	hypothetical prote
25	142	2.8	1186	2 T03180	tyrosine protein k
26	132	2.6	462	2 T36185	hypothetical prote
27	127	2.5	1820	2 A55494	latent transformin
28	123.5	2.5	454	2 A46498	glucocorticoid-sen
29	122	2.4	1374	2 S70712	protein-tyrosine k

30	121.5	2.4	2471	2 T03820	probable histidine
31	121	2.4	1888	2 T39009	hypothetical prote
32	119.5	2.4	475	2 A38340	66k glycoprotein p
33	119	2.4	2019	1 JQ1322	tenascin precursor
34	117	2.3	335	2 T11588	nuclease NUC1 (EC
35	116.5	2.3	989	2 S69711	hypothetical prote
36	112	2.2	1035	2 S61342	sulfite reductase
37	112	2.2	1394	2 A35626	transforming growt
38	112	2.2	2911	2 T20566	hypothetical prote
39	111	2.2	1394	2 A29637	position-specific
40	111	2.2	3002	2 A47221	fibrillin 1 precur
41	110.5	2.2	2871	2 A55567	fibrillin 1 - bovi
42	110.5	2.2	3147	2 T18674	hypothetical prote
43	110	2.2	753	2 T28787	hypothetical prote
44	109.5	2.2	476	1 SGMSV	vitronectin precu
45	109.5	2.2	1472	2 S67195	probable membrane

ALIGNMENTS

RESULT 1
A55144
autotaxin precursor - human
N:Contains: phosphodiesterase I (EC 3.1.4.1)
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A55144; A42329
R:Murata, J.; Lee, H.Y.; Clair, T.; Krutzsch, H.C.; Arestad, A.A.; Sobel, M.E.; Liott
J. Biol. Chem. 269, 30479-30484, 1994
A:Title: cDNA cloning of the human tumor motility-stimulating protein, autotaxin, rev
A:Reference number: A55144; MUID:95074054
A:Accession: A55144
A:Molecule type: mRNA
A:Residues: 1-915 <MUR>
A:Cross-references: GB:L35594; NID:g537905; PIDN:AAA64785.1; PID:g537906
A:Note: parts of this sequence were confirmed by peptide sequencing
R:Stracke, M.L.; Krutzsch, H.C.; Unsworth, E.J.; Arestad, A.; Cioce, V.; Schiffmann,
J. Biol. Chem. 267, 2524-2529, 1992
A:Title: Identification, purification, and partial sequence analysis of autotaxin, a
A:Reference number: A42329; MUID:92129337
A:Accession: A42329
A:Molecule type: protein
A:Residues: 256-266; 422-444; 504-507, 'AN'; 510, 'X'; 511-515; 533-548; 'S', 554-559, 'N', 561-
A:Experimental source: A2058 melanoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:78526, NCBIP:78523, NCBIP:78521,
A:Note: a peptide fragment Tyr-Asp-Val-Pro-Irp-Asn-Glu-Thr-Ile was also found
C:Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.
C:Genetics:
A:Gene: GDB:ATX
A:Cross-references: GDB:378346
A:Map position: 8q22-8qter
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase
F:55-98/Domain: somatomedin B homology <SBH1>
F:99-142/Domain: somatomedin B homology <SBH2>
F:54,463,577,859/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:210/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 100.0%; Score 5019; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSFQSCQIISLFTFAVGVSGICLGFTHRIKRAEGWEEGPPPTVLSDSPWTNISGCK 60
|||||
Db 1 MARRSFQSCQIISLFTFAVGVSGICLGFTHRIKRAEGWEEGPPPTVLSDSPWTNISGCK 60

QY 61 GRCFELQAGPPDCDNLCKSYSCCHDFDELCLKTARGWECTKDRGGEVRNEENACHC 120
|||||

Db 61 GRCFELQAGPPDCDNLCKSYSCCHDFDELCLKTARGWECTKDRGGEVRNEENACHC 120

QY 121 SEDCLARGDCCTNYQVVKGESHWDDDCCEIKAAECPAGFVRPPLIIFSVGDGFASYMK 180

|||||
Db 121 SECLARGDCTNYQVVKESHWDDECEIKAECPAGFVRPLLIIFSVDFRSTWK 180
QY 181 KGSVMPNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPVFDA 240
Db 181 KGSVMPNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPVFDA 240
QY 241 TFHLRGREKNHRWGGQPLWITATKQGVKAGTFWVVIPIHERRILTLRLWLDPDR 300
Db 241 TFHLRGREKNHRWGGQPLWITATKQGVKAGTFWVVIPIHERRILTLRLWLDPDR 300
QY 301 PSYAFSEQDFSGHKYGFPGPESSVSGSFTPAKPKRVKAPKROERVPAPPKRRR 360
Db 301 PSYAFSEQDFSGHKYGFPGPESSVSGSFTPAKPKRVKAPKROERVPAPPKRRR 360
QY 361 KHRMDHYAETRODKMTNPLREIDTKIVGQMDGLKQLKLRRCVNVIFVGDHGMEDVTC 420
Db 361 KHRMDHYAETRODKMTNPLREIDTKIVGQMDGLKQLKLRRCVNVIFVGDHGMEDVTC 420
QY 421 RTEFLSNLYTNVDDITLVPGLGRIRKFSNNAKYDPAKIIANTCKKPDQHFYLPKQH 480
Db 421 RTEFLSNLYTNVDDITLVPGLGRIRKFSNNAKYDPAKIIANTCKKPDQHFYLPKQH 480
QY 481 LKRLHYANNRRRIEDHLLVERRHVARKPLDVYKPSGKCFQGDHGFNDKVNMSQTVF 540
Db 481 LKRLHYANNRRRIEDHLLVERRHVARKPLDVYKPSGKCFQGDHGFNDKVNMSQTVF 540
QY 541 VGYGPTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLTLNTFRPTMPEV 600
Db 541 VGYGPTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLTLNTFRPTMPEV 600
QY 601 TRNYPGIMYLSQDFDLGCTDDKVEPKNKDELNKLRLHTKGTSTEEHLLYGRPAVLRYT 660
Db 601 TRNYPGIMYLSQDFDLGCTDDKVEPKNKDELNKLRLHTKGTSTEEHLLYGRPAVLRYT 660
QY 661 RYDILYHTDESYSSEIFLMLLTSTYVSKQAEVSSVPDHLTSCVRPDRVSPSQNCL 720
Db 661 RYDILYHTDESYSSEIFLMLLTSTYVSKQAEVSSVPDHLTSCVRPDRVSPSQNCL 720
QY 721 AYKNDKMSYGFLLPPYLSSSPEAKYDAFLVTNMVPMYPAKRVNMYFORVLVKKYASER 780
Db 721 AYKNDKMSYGFLLPPYLSSSPEAKYDAFLVTNMVPMYPAKRVNMYFORVLVKKYASER 780
QY 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPHYYSIITSCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPHYYSIITSCLDFTQPADKCDGP 840
QY 841 LSVSSFTLPHRPNDEESCNSEDESKWVEELMKHMTARVRIEHLTSLDFFRKTSRSTPE 900
Db 841 LSVSSFTLPHRPNDEESCNSEDESKWVEELMKHMTARVRIEHLTSLDFFRKTSRSTPE 900
QY 901 ILTLKTYLHTYESEI 915
Db 901 ILTLKTYLHTYESEI 915

RESULT 2

A55453
plasma cell membrane glycoprotein PC-1, brain specific - rat
N:Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A55453; J00187
J:Ratita, M.; Goji, J.; Nakamura, H.; Sano, K.
J: Biol. Chem. 269, 28235-28242, 1994
A:Title: Molecular cloning, expression, and localization of a brain-specific phosphodiesterase I (EC 3.1.4.1)
A:Reference number: A55453; MUID:95050605
A:Accession: A55453
A:Molecule type: mRNA
A:Residues: 1-885 <NAR>
A:Cross-references: GB:D28560; NID:g464196; PIDN:BAA05910.1; PID:g464197
R:Narita, M.; Goji, J.; Sano, K.; Nakamura, H.
submitted to JIPID, February 1994

A:Description: Cloning and expression of brain-specific nucleotide diphosphohydrolase
A:Reference number: J00187
A:Accession: J00187
A:Molecule type: mRNA
A:Residues: 1-66, 'Q', 68-81, 'T', 83-94, 'C', 96, 'A', 98-195, 'A', 197-514, 'E', 516-621, 'E', 62
A:Experimental source: strain Sprague-Dawley
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphoric diester
F:54-97/Domain: somatomedin B homology <SBH1>
F:98-141/Domain: somatomedin B homology <SBH2>
F:53,150,396,408,522,608,829/Binding site: carboxylate (Asn) (covalent) #status pred
F:207/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 85.8%; Score 4306; DB 1; Length 885;

Best Local Similarity 83.6%; Pred. No. 1.7e-287;

Matches 792; Conservative 33; Mismatches 28; Indels 94; Gaps 6;

QY 1 MARRSFQSCIIISLFTFAVGVISICLGTFAHRIKRAEGWEEGPTVLSOSPWTNIGSCK 60
Db 1 MARQGLGSFQVISLFTFAISVNICLGTASRIKRAE-WDEGPTVLSOSPWTNIGSCK 59
QY 61 GRCELOEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRSGEVNNEACHC 120
Db 60 GRCELOEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRSGEVNNEACHC 119
QY 121 SEDCLARGDCTNYQVVKESHWDDECEIKAECPAGFVRPLLIIFSVDG 173
Db 120 PEDCLSRGDCCTNYQVVKESHWDDECEIKAECPAGFVRPLLIIFSVDG 170
QY 174 FRASYMKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSM 233
Db 171 FRASYMKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSM 230
QY 234 YDPVDFATPHLGRKFNHRWGGQPLWITATKQGVKAGTFWVVIPIHERRILTLRLWL 293
Db 231 YDPVDFATPHLGRKFNHRWGGQPLWITATKQGVKAGTFWVVIPIHERRILTLRLWL 290
QY 294 TLPDHERPSVAFYSEQDFSGHKYGFPGPESSVSGSFTPAKPKRVKAPKROERVA 353
Db 291 SLPDNERPSVAFYSEQDFSGHKYGFPGPESSVSGSFTPAKPKRVKAPKROERVA 351
QY 354 PKPKRRRKLTHMDHYAETRODKMTNPLREIDTKIVGQMDGLKQLKLRRCVNVIFVGDH 413
Db 322 -----MTNPLREIDTKIVGQMDGLKQLKLRRCVNVIFVGDH 358
QY 414 MEDVTCDRTEFLSNLYTNVDDITLVPGLGRIRKFSNNAKYDPAKIIANTCKKPDQHF 473
Db 359 MEDVTCDRTEFLSNLYTNVDDITLVPGLGRIRKFSNNAKYDPAKIIANTCKKPDQHF 418
QY 474 KPYLKHLPKRLHYANNRRRIEDHLLVERRHVARKPLDVYKPSGKCFQGDHGFNDKV 533
Db 419 KPYMKHLPKRLHYANNRRRIEDHLLVDRRHVARKPLDVYKPSGKCFQGDHGFNDKV 478
QY 534 NSMQTVFVGYGPTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLTLNTFR 593
Db 479 NSMQTVFVGYGPTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLTLNTFR 538
QY 594 PTMPDEVPNYPGIMYLSQDFDLGCTDDKVEPKNKDELNKLRLHTKGTSTEEHLLY 645
Db 539 PTMPDEVPNYPGIMYLSQDFDLGCTDDKVEPKNKDELNKLRLHTKGTSTEEHLLY 598
QY 646 -----ERHLLYGRPAVLRYTIDYHTDESYSSEIFLMLLTSTYV 688
Db 599 SKHENKKNLNGSVPEPKRHLHYGRPAVLRYTIDYHTDESYSSEIFLMLLTSTYV 658
QY 689 SKQAEVSSVPDHLTSCVRPDRVSPSQNCLAYKNDKMSYGFLLPPYLSSSPEAKYDA 748
Db 659 SKQAEVSSVPDHLTSCVRPDRVSPSQNCLAYKNDKMSYGFLLPPYLSSSPEAKYDA 718
QY 749 FLVTNMVPMYPAKRVNMYFORVLVKKYASERNGVNVISGPIFDYDGLHDTEDKIKQY 808
Db 719 FLVTNMVPMYPAKRVNMYFORVLVKKYASERNGVNVISGPIFDYDGLHDTEDKIKQY 778

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QY 809 VEGSSIPVTHYYSIIITSCLDFTQPADKCDGPLSVSFFILPHRPDNEESCSNSEDSESKW 868
Db 779 VEGSSIPVTHYYSIIITSCLDFTQPADKCDGPLSVSFFILPHRPDNEESCSNSEDSESKW 838
QY 869 EELMKHMTARVRDIEHLTSLDFRKTSGSPETLTILTKYLYHTYESEI 915
Db 839 EELMKHMTARVRDIEHLTSLDFRKTSGSPETLTILTKYLYHTYESEI 885

RESULT 3
A57080
cell surface antigen R813-6 - rat
N:Contains: phosphodiesterase I (EC 3.1.4.1)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A57080
R:Deissler, H.; Lottspeich, F.; Rajewsky, M.F.
J. Biol. Chem. 270, 9849-9855, 1995
A:Title: Affinity purification and cDNA cloning of rat neural differentiation and tumor
A:Reference number: A57080; MUID:95247775
A:Accession: A57080
A:Status: preliminary
A: Molecule type: mRNA
A:Residues: 1-875 <DE>
A:Cross-references: GB:247987; NID:g806378; PIDN:CAA88029.1; PID:g806379
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase; sud
F:1-22/Domain: cytosolic #status predicted <CYT>
F:23-45/Domain: transmembrane #status predicted <TM>
F:46-875/Domain: extracellular #status predicted <EXT>
F:51-94/Domain: somatomedin B homology <SBH>
F:95-138/Domain: somatomedin B homology <SBH2>
F:206/Binding site: AMP (Thr) (covalent) #status predicted
F:237,280,289,533,574,594,702,789/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 41.5%; Score 2084; DB 1; Length 875;
Best Local Similarity 43.5%; Pred. No. 5e-135;
Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;

QY 57 GSKCGFELQAGPPDCRDNLSKYSCTCHDFDELCLKTARGWECTKDRCGEVNEN 116
Db 53 GCRKRCDSHRRLEGKCDGCDGDRGCCWDFCTVKSTQITCNFSRCGETLEAA 112
QY 117 ACHSEDCLARGDCCTNYGVCKGESHVDDDCCEIEKAAECFAGFVRPPLIIFSVDFRA 176
Db 113 LSCADDCLQRKDCCTDYKAVCGEVPWTEACASSQEQCPGFPQPPVILFSDGFA 172
QY 177 SYMKKGKVMPIEKLRSCTGHSYMRPVYPTKTPNLYTLATGLYPESHGIYGNMYDP 236
Db 173 EYLQWSTLLPNINKLCTGLSKYMRAMPYPTKTPNHYTIVTGLYPESHGIIDNNYDV 232
QY 237 VDATFHLGRGKFNHRWGGPPLWITATKQGVKAGTFFW-----SV 278
Db 233 YLNKFSLSSEKSNAPMWSGQPIWLTAMYQGLKAASYWLGSDVAVNGSFPPNIYRNS 292
QY 279 VIPHERILLTLRWLTLPDHERPSVAFYSEQPDFSGHRYGPGPPESSVSGSPFTAKRP 338
Db 293 SVPYESRTATLQWLQDLKFAERPSYTYIVEPDSAGHSGPV-----SAG 338
QY 339 KRKVPKRQRPVAPPKRRRKIRHMDHYAAETRODKMTNPLREIDKVLQGLMDGLKQL 398
Db 339 -----VIKALQLVDDAFGLMEGLKQR 360
QY 399 KLRCCNVIFVGDHGMEDVTCRTBELSNLYNVDITLVPGLGRISK-----FSNN 452
Db 361 NLHNCVNIIVLADHGMQDTSQDRVEYMTDYFPEI-NFYMQGPAPRIARNIPQDFFTN 419
QY 453 AKYDPKAIANTLCKPQDHFQPKYLQHLPLKRLHYANNRIEDIHLLVRRHWVARKPLD 512
Db 420 S-----EIVRDLSCRSDQHFQPKYLPDLPKRLHYAKNVRIDKVLHMLVDROWLAYR--- 471
```

```
QY 513 VYKPSGCKFFQGDGFDKNVSNMQTVFVGYPGPTFKYKTKVPPFENIELYNVMDLLGLK 572
Db 472 --NKGSSNC-EGGTHGYNNEFKSMEALFLAHGPPSFKEKTVIEPFENIEVYNLLCDLLHIQ 528
QY 573 PAPNNGTHGSLNHLRTNFRPTMPEEVTFRPNYPCIMYQLQSDFDLGCCTCDKVEPKNLD 632
Db 529 PAPNNGSHGSLNHLKAPFYQPSHAELSLSKAGCGFTTLPKDSLNCSC-LALQTSQGE 587
QY 633 ELNRLHTKG----STEERHLLYGRPAVLYRTR-YDILYHTDFESGYSEIFILMLWTSYT 687
Db 588 QVNQRLNLSGGEVATEKTNLPGFRPRVIOKNKDCHLLYHREYVSGFGKMKMPMWSYT 647
QY 688 VSKQAEVSSVPDHLTSCVRPDRVSPSPSONCLAYKNDQMSYGFPLFPYSSSPKAYD 747
Db 648 VPKPGDTSLSLPTVPDCLRADRVDPSESQKCSFYLDQNDIDHGFLYPPAIGNNESQYD 707
QY 748 AFLVTNVMYPAKRYVMYFORVLVKYASERNGVVISGPIFDYDGLDHTEDKIKQ 807
Db 708 ALITSNLMVPMKEFKMWDYFHKVLLIKYAIERNGVNVVSGPIFDYDGHFDAPDEITN 767
QY 808 YVEGSSIPVTHYYSIIITSCLDFTQPADKCDGPLSVSFFILPHRPDNEESCSNSEDSESKW 867
Db 768 YVAGTDVPVTHYFVLTSCNKTHTPDCPGWLDVLPFVVPVPHRPTNVESCPENKAEDLW 827
QY 868 VEELMKHMTARVRDIEHLTSLDFRKTSGSPETLTILTKYLYHTYESEI 915
Db 828 VEERFKAHARVRDVELLTGLDFYQKTPQVSEILQLKTYLPTETII 875

RESULT 4
A39216
plasma cell membrane glycoprotein PC-1 - human
N:Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C:Accession: A39216; S21706; S23587; S51030
R:Buckley, M.F.; Loveland, K.A.; McKinsty, W.J.; Garson, O.M.; Goding, J.W.
J. Biol. Chem. 265, 17506-17511, 1990
A:Title: Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule,
A:Reference number: A39216; MUID:91009202
A:Accession: A39216
A:Status: preliminary
A: Molecule type: mRNA
A:Residues: 1-925 <BUC>
A:Cross-references: GB:J05654
R:Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S
Arch. Biochem. Biophys. 295, 180-187, 1992
A:Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase.
A:Reference number: S21706; MUID:92246539
A:Accession: S21706
A:Status: not compared with conceptual translation
A: Molecule type: mRNA
A:Residues: 1-925 <FUN1>
A:Accession: S23587
A: Molecule type: protein
A:Residues: 116-121;247-271,'X',273-275;279-280,'X',282-283;303-316;362-364;449-465;4
A:Note: it is uncertain whether Met-1 or Met-53 is the initiator
R:Belli, S.I.; Goding, J.W.
Eur. J. Biochem. 226, 433-443, 1994
A:Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline ph
A:Reference number: S51030; MUID:95094801
A:Accession: S51030
A:Status: preliminary
A: Molecule type: mRNA
A:Residues: 1-80 <BEL>
C:Genetics:
A:Gene: GDB:PDNPI; M6S1; NPPS
A:Cross-references: GDB:132615; OMIM:173335
A:Map position: 6q22-6q23
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; t
F:77-97/Domain: transmembrane #status predicted <TM>
```

F:104-144/Domain: somatomedin B homology <SBH1>
F:145-188/Domain: somatomedin B homology <SBH2>
F:179,285,341,477,578,585,643,700,731,748/Binding site: carbohydrate (Asn) (covalent) #s
F:256/Binding site: AMP (Thr) (covalent) #status predicted

```
Query Match          39.08; Score 1955.5; DB 1; Length 925;
Best Local Similarity 42.28; Pred. No. 3.5e-126;
Matches 378; Conservative 150; Mismatches 252; Indels 115; Gaps 19;

QY  58  SCKGRCELOEAGPPDCRCNLCYSYSCCHDFELCLKTARGWECTKRCGEVRENEA 117
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 107  SCKGRCEP-RTFG--NCRCDACVGLNCLDYOETCLEPHIWTCKNRCGEKRLTSL 163
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 118  CHCEDCLARGDCCTNYQVCKGSHWDDCEIEKAECAPAGFVRPLLIIFSVDFGRAS 177
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 164  CACSDCKDKGDCINYSVQCKGKSWEEPCEINQPCPAGFPTPTLLFLSLDGFRAE 223
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 178  YMKGSKVMPNIEKLKSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPV 237
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 224  YLHTWGGLLPVISLKKCGTGTKNMRPVYPTKTPNHYSTVGLYPESHGIDNKMDPK 283
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 238  FDATFHLRGREKFNHRWGGOPLTATKQGVKAGTFEF-----SVV 279
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 284  MNASFSLSKSEKFNPEWKGEPIWYAKYQGLKSGTFWPGSDVEINGIFPDYKMYNGS 343
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 280  IPHERRILTLRWLTLPDHERPSVYAFYSEQDFSGHKYGFPGPESSYSGSPFTPAKRPK 339
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 344  VPFEERILAVLQWLQPKDRPHEFTYLYLEEDSSGSHGVPVSSE----- 388
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 340  RVAPKRRQERVPAPPKRRRKIRHMDHYAAETRODKMTNPLREIDKIVQMLDGLKQLK 399
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 389  -----VIKALQKRVDMVGMGLDKELN 411
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 400  LRRCVNVIFVGDHGMEDVTCDRTEFLSNLYTNVDDITLVPGLTGRIR-----SKFSNNAK 454
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 412  LHRCLNLLISDHGMEQSGCKKYLYLNKLGVDVKNIKVYIPGAARLSDVPDKYIS--- 468
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 455  YDPKAIITANLTKCKPDQHFYKPLKQHLFRLHYANNRRIEDIHLVERHWVARKPLDVIY 514
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 469  FNYEGIARNLSCREPNQHFYKPLKQHLFRLHYANNRRIEDIHLVERHWVARKPLDVIY 514
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 515  KPSPGCKFFQDGHGFDKNVNSQVTFVGVGPTFYKTKVPPFENTELNVNMDLGLKLPK 574
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 527  RKYCG----SGFHGSDNVFSNMQALFVGVGPKFKGIEADTFENIEVYNLMCDLNLTPA 582
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 575  PNNTHGSLNHLTLNTFRPTMPEVTRPNYPGIMYLOSDF-----DLGCTCDKVEPK 628
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 583  PNNTHGSLNHLTLNPVTPKHPREV----HP--LVQCPTRNPRDLNLCSCNPSILP- 634
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 629  NKLDENAKRLHTKGTSEE--RH--LLXGRPAVLXR-TRYDILYHDFESGYSEIFLMLIW 683
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 635  --IEDFQTFNLTVAEKIIKHETLPYGRPVQLKENTICLLSQHFNHSGYSQDILMPLW 692
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 684  TSYTVSQAEVSSVDDHLTSCVRDVRVSPFSQNLAYKNDKQMSYGLPPLPPYSSSPE 743
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 693  TSYTVDRNDSEST--EDFSNCLYQDFRPLSPVHKCFYKNNKTVSYGFLSPQLNKSS 750
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 744  AKY-DAFLVTNMPVPAFKRVNRYFORVLVKYASERNGVNVISGPTFDYDYGDLHDE 802
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 751  GIYSEALLTNVPMYQSFQVIWRYFHTLLRKYAERNGVNVSGPVDFDYGDCDLSL 810
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 803  DKIKQ----YVGESSIPVTHYISITSCDTPQADKCDGPLSVSSFILPHRPDNEECN 859
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 811  ENLRKRRVIRNQELIPTHFFIVLTSCDTSQTPHLCEN-LDTLAFILPHRTDNSESCV 869
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 860  SSEDESKWVELMKMHTARVDRDIEHLTSLDFRKTSTRSYPEILLTKTYLHYESE 914
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 870  HGKHDSSWVEELLHRRARITDVEHITLSFYQOKPEVPSDILKLTHTLPTFSQE 924
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
```

RESULT 5
A27410

plasma cell membrane glycoprotein PC-1 - mouse
N:Alternate names: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C:Accession: A27410; I59055; S38354
R:van Driel, I.R.; Goding, J.W.
J. Biol. Chem. 262, 4882-4887, 1987
A:Title: Plasma cell membrane glycoprotein PC-1. Primary structure deduced from cDNA
A:Reference number: A27410; MUID:87165906
A:Accession: A27410
A:Molecule type: mRNA
A:Residues: 1-905 <VAN>
A:Cross-references: GB:J02700; NID:g200236; PIDN:AAA39893.1; PID:g200237
A:Note: The authors translated the codon CAG for residue 24 as Glu
R:van Driel, I.R.; Wilks, A.F.; Pietersz, G.A.; Goding, J.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8619-8623, 1985
A:Title: Murine plasma cell membrane antigen PC-1: Molecular cloning of cDNA and anal
A:Reference number: I59055; MUID:86094275
A:Accession: I59055
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 203-219 <RES>
A:Cross-references: GB:M12552; NID:g200234; PIDN:AAA39892.1; PID:g200235
R:Belli, S.I.; van Driel, I.R.; Goding, J.W.
Eur. J. Biochem. 217, 421-428, 1993
A:Title: Identification and characterization of a soluble form of the plasma cell mem
A:Reference number: S38354; MUID:94039066
A:Accession: S38354
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 35-219 <BEL>
A:Cross-references: EMBL:L04516
C:Genetics:

A:Introns: 62/3; 87/1; 126/1; 168/1; 188/2
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: coenzyme A; glycoprotein; phosphoric diester hydrolase; t
F:86-126/Domain: somatomedin B homology <SBH1>
F:127-170/Domain: somatomedin B homology <SBH2>
F:161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predict
F:238/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 37.8%; Score 1899.5; DB 1; Length 905;
Best Local Similarity 41.0%; Pred. No. 2.4e-122;
Matches 365; Conservative 155; Mismatches 262; Indels 109; Gaps 16;

```
QY  58  SCKGRCELOEAGPPDCRCNLCYSYSCCHDFELCLKTARGWECTKRCGEVRENEA 117
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db  89  SCKGRCFERTFS---NCRDAAACVSLGNCLDPQETCEPETHIWTCKNRCGEKRLSRFV 145
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 118  CHCEDCLARGDCCTNYQVCKGSHWDDCEIEKAECAPAGFVRPLLIIFSVDFGRAS 177
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 146  CSCADDCKTHNCCINYSVQCKDKSWETCESIDTPECPAEFESFPILLFLSLDGFRAE 205
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 178  YMKGSKVMPNIEKLKSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPV 237
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 206  YLHTWGGLLPVISLKKCGTGTKNMRPVYPTKTPNHYSTVGLYPESHGIDNKMDPK 265
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 238  FDATFHLRGREKFNHRWGGOPLTATKQGVKAGTFEF-----SVV 279
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 266  MNASFSLSKSEKFNPLMYKQPIWYTAHNOEVKSGYFWPGSDVEIDGILPDYIKVYNGS 325
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 280  IPHERRILTLRWLTLPDHERPSVYAFYSEQDFSGHKYGFPGPESSYSGSPFTPAKRPK 339
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 326  VPFEERILAVLQWLQPSHERPHFTYLYLEEDSSGSHGVPVSSE----- 370
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 340  RVAPKRRQERVPAPPKRRRKIRHMDHYAAETRODKMTNPLREIDKIVQMLDGLKQLK 399
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 371  -----VIKALQKRVDRVLGMLDGLKDLG 393
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :

QY 400  LRRCVNVIFVGDHGMEDVTCDRTEFLSNLYTNVDDITLVPGLTGRIRSFNSNAKY--DP 457
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
Db 394  LOKCLNLLISDHGMEQSGCKKYLYLNKLGVDVNNVYVYGAARLRPTDVPETYSFNY 453
    |||||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :  :|||  :
```

	364	RMDHYAAETRODKMNTPLREIDTKIVGOLMDGLKQLKLRCVNVIFVCDHGCMEDVTCDRTE	423
Qy			
	231	-----RVTEAVSKVDKMIGRIIMGLEKKRFVSDFHVILLJGDHGW----TNCDDKV	277
Db			
	424	FLSNLYLNMVDITLVPG-----TLGR-IRSFESNNAKYDPKAIITANLTCK	468
Qy			
	278	I---YIDDLADWIKIPADWIQDYSVPULAMPNGKGVKNPQGKNAELUVRKMEALSISGKV	334
Db			
	469	PDOHF-KPYLKQHLPKRLLHYANNRRIEDIHLLVERRHVAARKPLDYVKPKSCFFQGDH	527
Qy			
	335	ANGFELQVYLKENLPQRLLHYSDDSRIPPIIGMWCEGLWKQNTYYQ-----EC--SGTH	387
Db			
	528	GFDKNVNSMTQTVFYGYPTFKYTKTPPPENIELYNVMCOLLGLKLPAPNNGT	579
Qy			
	388	GYDNMFMSRISIFYGYPRFRRGKIKPFNFNNVOVNVAEILGLRAPNNGS	439
Db			

RESULT 7
T09931
nucleotide pyrophosphatase homolog T16L4.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C;Accession: T09931

A:Reference number: Z16897
A:Accession: T09931
A:Molecule type: DNA
A:Residues: 1-496 <EV>
A:Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190
A:Experimental source: cultivar Columbia; BAC clone T16L4
C:Genetics:
A:Gene: ATSP:T16L4.190
A:Map position: 4

[illegible]

QY 322 GPRESSUSFTPAKRPKRKVAPKRQERPVAPKRKRRIHRMDHYAAETRQDKMTNPL 381
Db 281 DPQ-----ITEAV 288

```

QY 382 REIDQVQLMDGLGKQDKLRRCVNVIFVGDHGMEDVTCORTEFLSNLYLNIVDDIT---LV 433QY
    ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 289 VNIDRLGRLIDGLEKRGIFEDVTMIWGDHGMVG--TCDKK-----LVVDDLPAPWIKI 341
    ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY 439 PGT-----LGRIRSFSSNNAKYDPKAITANTLCTCKPD--QHFKPYLQKHLPKRLHYAN 489
    ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 342 PSSWQVYTPPLAIQPPSGHDAADIIVAKINEGLSSKGVENGRYKLYLVEDLPSRLHYVD 401
    ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY 490 NRRIEDIHLVERRRHWARRPLDVYKPKSKCFQFGDHGFDKNVNSMQVTFVGYGPTFKY 549
    ||||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 402 SDRIPPIIGLVDEGFKVEQK-----KSKAKEC--GGAHGYDNAFFSMRTIFIGHGPMESK 454
    ||||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY 550 KTKVPPPEINELYNVMDLGLGLKPAPNNGT 579
    ||||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 455 GRKVPSPENQIYNVISSILGLKAAPNNGS 484
    ||||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

```

RESULT 8

T03293
nucleotide pyrophosphatase homolog - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
R:Hsing, Y.C.; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.
submitted to the EMBL Data Library, April 1995
A:Description: Rice early embryogenesis gene.
A:Reference number: Z14889
A:Accession: T03293
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-479 <HSI>
A:Cross-references: EMBL:U25430; NID:g818848; PID:g818849
A:Experimental source: strain Tainung 67
C:Genetics:
A:Note: OSF4

Query Match 12.2%; Score 611.5; DB 2; Length 479;
Best Local Similarity 31.4%; Pred. No. 2.5e-34;
Matches 150; Conservative 65; Mismatches 132; Indels 131; Gaps 14;
QY 152 IKAECAGFVR-----PPLIFSVDFPRASYMKKSKVMPNTEKLRSCGTHSPY-MR 203
DB 71 LSAAPAPAAARAQVKLEKPVYILLISDFRFGYQHAA--TPHIRLIGNGTSAAATGLV 128
QY 204 PVYPTKFPNLYLATGLYPESHGIVGSMYDVPDADFHLGRKFNHRWGGGLOPLMIT 263
DB 129 PIFTLIFPNHYSATGLYPSSHGIINNYFPDPISGDIYFTSSHEP---KWLGEPLMWT 185
QY 264 ATKGVKAGTFW-----SVVIPHERRILTLRWLTLPDHERPSV 303
DB 186 AADQGIQAATVFPGESEVKGSWDCPKYCRHNGSVFPEERVDAILGVDFLPSDEMPQF 245
QY 304 YAFSEQPDPSGHYKYPGPPRESSYGSPTTAKRPRKRVAPKRRQRPVAPPKRRKIH 363
DB 246 LTLVDFPDHGHQVQDDP----- 265
QY 364 RMDHYAAETRODKMTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDHGMEDVTCR-- 421
DB 266 -----AITEAVRIDEIGRIAGLEERGVEDVNVILVGHGWG-TCDKKL 312
QY 422 -----TEFLSNLYTNVDDITLVPGLTGRIRSKFSNNAKYDPKAI 461
DB 313 VFLDELAPWIKLEEDWLSMTPLLA--IRPPDMSL-PDVAKMNEGLSGK-----V 362
QY 462 ANLTCKPDQHKPYLQKHLKRLHYANNRIEDTHLLVERHWHVARKPLDVKYKPSGKC 521
DB 363 EN-----GEYLRMYLKEDLPSRLHYADSYRIPPIIGLPEEGYKVKMRSD--KNECG-- 412
QY 522 FFGDGHGDNKVNVMOTVFVGYGPTFKYKTVPPPEINTELYNVMCDLLGLKPPANNGT 579
DB 413 ---GAHGVDNAFFSMRTIFIAHGRFREGVRVVPSENVFIYNVIAISILNLEPAPNNGS 467

RESULT 9

T19494
hypothetical protein C27A7.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19494
R:Harris, B.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19132
A:Accession: T19494
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-829 <WTL>
A:Cross-references: EMBL:Z81041; PIDN:CA802784.1; GSPDB:GN00023; CESP:C27A7.1
A:Experimental source: clone C27A7
C:Genetics:

A:Gene: CESP:C27A7.1

A:Map position: 5
A:Introns: 12/3; 37/1; 100/3; 176/2; 272/3; 392/1; 427/1; 479/2; 566/2; 588/3; 677/1;

Query Match 12.2%; Score 610; DB 2; Length 829;

Best Local Similarity 23.9%; Pred. No. 6.5e-34;
Matches 192; Conservative 127; Mismatches 278; Indels 208; Gaps 31;
QY 139 KGESHVWDDDCERIKAAECPAGFVRPPLIFSVDFGRASYMKKSKVMPNIEKLRSCGTH 198
DB 158 KARYEW--KGCQNLGKCEL--SGYTKPPLVILSLDGPAREYVDR--NIVQFLNIADCGVK 212
QY 199 SPYMRPVYPTKFPNLYLATGLYPESHGIVGSMYDVPDADFHLGRKFNHRWGGG 258
DB 213 ADKVPSYSPKTFPNHYSIVTGLWPESHGITDINSVDPTISPVLESKMSTKY-EKFEFE 271
QY 259 PLW-ITATKQGVKAGTFW-----SVVIPHERRILTLRWLTLPDHE 299
DB 272 PWSVYKRTKGGKCANCLFWVGCAVNSGYAPADVAPAYNQELPFRNIDTVEWLKLPVDE 331
QY 300 RPSVAFYSEQPDPSGHYKYPGPPRESSYGSPTTAKRPRKRVAPKRRQRPVAPPKRR 359
DB 332 RGLITAYLHEPDNAGH----- 348
QY 360 RKIHRMDHYAAETRODKMTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDHGMEDVTC 419
DB 349 ---YQVD-----EEDVDEKLAIEDENLDYLSRLSEKLECFINFAILSDHGMQLI-- 396
QY 420 DRTEFLSNLYTNVDDITLVPGLTGRIRSKFSNNAKYDPKAIANLTCKKPDQHKPYLQK 479
DB 397 DKTYYPQDYL-DLKLITAKGVVGRV---YINDTISVNDVDVKFRCK--IDAVKTNTRS 450
QY 480 HLPKRLHYANNRIEDTHLLVERHWHVARKPLDVKYKPSGKCFQGDHGFNDKVNVMOTV 539
DB 451 DVPTRKHYSRDPVGEV--LLE-----GRAGVTFYKSKADDYELSGDHGVDYFNPKMHTI 503
QY 540 FVGYGPTFKYKTVPPPEINTELYNVMCDLLGLKPA--PNNGTHGSLNHLRLTFRPTMPE 598
DB 504 FVARGSPKQNTTISPQNIQYMNLMNLGIEGAVETNCTIGFFDNIL--TNPPRRDNPT 562
QY 599 EVTRP-----NYPGIMVLOSDFLGCTCDDKVEPKNLDELKRLHKGSTGEERHLLYGRP 654
DB 563 NVIGECPIAFAFSV-----LKCSGNVSAETLNQL-----SVKLNCAFSPT 603
QY 655 AV-LYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQA-----VSSVSPDH 700
DB 604 NPLYSNHCFFQNYCD-----NSVLYSRKGNDAARRAIEVLSRDEASNPNS 649
QY 701 LTSCVRPVRVSPFSQNC-----LAYKNDKQMSYGLFPPYLSSSPEAKYDA---F 749
DB 650 FTF-----LNKQYQSNCPSHIPTGSLTIRONSQ-----LSSMYDERIDVPNNF 692
QY 750 LVTNVPMTPAFKRVWNYFORVLVKYASERNGVNIVISGPIFYDYDGLDHTDEKIKQYV 809
DB 693 LLKVLDPLOAKSMEXLNKFKGMV-----VISGTATDINHDIADS----- 732
QY 810 EGSSIVPPTHYSIITSC---LDFTQPADKCDGPLSVSSSIFLPHRPDNEESCNSSEDES 865
DB 733 NGSVI---THIYRIMLICNSTWLLMNPPLCTDSDSMDTLFSFIPTQEQSDICMSSDD-- 787
QY 866 KWVEELMKMHTARVRDIEHLTSLDF 890
DB 788 ----ILLDYATATFDVERISGQF 807

RESULT 10

T09933
nucleotide pyrophosphatase homolog T16L4.210 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C:Accession: T09933
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.

QY 441 TLGRIRSKFSNNKAYDPKAIITANLTCKPDDHFPYKQLKHLPKRLHYANNRRIEDIHLV 500
 Db 291 AYAGIEPSSGSLK-DLEPLFAS-----HDHMCQWPKQIIPARFHYGONPRVPAVCA 343
 QY 501 ERRHVARPKLDVYKPKSGCKFFOGDHGFDNKNVSMOTVFVGYGTFYKVKVPFFENIE 560
 Db 344 EVGHSIMGD--DSMAWATK-----GNHGYNQTPMGALFIANGPAFOKHVKVIESMDNID 397
 QY 561 LYNVMDLLGLKAP 575
 Db 398 VOPLVAQVILKAP 411

RESULT 13
 B82537
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: B82537
 R:anonymous, The xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: B82537
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-433 <SIM>
 A:Cross-references: GB:AE004067; GB:AE003849; NID:g9107818; PIDN:AAF85396.1; GSPDB:GN001
 A:Experimental source: strain 9a5C
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 Submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.C.R.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF2599

Query Match 9.28; Score 461; DB 2; Length 433;
 Best Local Similarity 27.18; Pred. No. 4.6e-24;
 Matches 125; Conservative 65; Mismatches 152; Indels 120; Gaps 13;

QY 166 LIIFSVDGFRASYMKKSGKVPNTKLRSCGTHSPYMRPVYPTKFPNLYTLATGLYPES 225
 Db 40 LLLILDLGRADALEHGO--APQARLASGDGVHAWMTPTSPALTPNAYTLITGLRDPH 97
 QY 226 HGIYGNMIDPVDFATHLRGKFNH--RWGGQFPLWITATKQYKAGTFFW-----SVV 279
 Db 98 HGIVHNTMEDPLLGA-PESENGEALSIDGRWGGEPINWYSAEHAGHSATFLWPGSEASTA 156
 QY 280 -----TPHERRITILRWLTPDHERPSVYAFYSEQPDFSGHKYGPFGPEES 326
 Db 157 GTRPSRWYANKHSADTQITQALRWLNERGPDAPRLVILRFEQVNTAGNSEGDPSPQ-- 214
 QY 327 SYGSPFPAKRPKRVAPKRRQRPVAPPKRRRKIRHMDYAAETRODKWNTNPLREIDK 386
 Db 215 -----YAAVHM-----IDS 224
 QY 387 IVGQMDGLKOLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNLYTNVD-----DIT 436
 Db 225 AIGRLIDSLRQHGKLTDDIVIVSDGIIAPIGDHAVFLERIVQLSDVHVVSDDGVGLGIT 284

QY 437 LYPGTILGRIRSK-FSNNKAYDPKAIITANLTCKPDDHFPYKQLKHLPKRLHYANNRRIED 495
 Db 285 PLPGHESKYEAMLLGAHATYD-----C-----WRQALPTRWYHTGTHPRIFN 326
 QY 496 IHLVERRWH-----VARKPLDVYKPKSGCKFFOGDHGFDNKNVSMOTVFVGYGPTFK 548
 Db 327 IVQMHGEGNALSAAQITKRHPLOM-----CGSSGFDPMPLPSMRAIFLANGPSEW 376
 QY 549 YKTKVPPFENIELYNVMDLLGLKAPNPNRGTHGSLNHLRTN 590
 Db 377 PNLLNPNINVDVYPLLTRLLGTAMAPNDGNPRALLQALRSS 418

RESULT 14
 T19495
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19495
 R:Harris, B.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19132
 A:Accession: T19495
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-674 <WILL>
 A:Cross-references: EMBL:Z81041; PIDN:CAB02785.1; GSPDB:GN00023; CESP:C27A7.3
 A:Experimental source: clone C27A7
 C:Genetics:
 A:Gene: CESP:C27A7.3
 A:Map position: 5
 A:Introns: 61/1; 98/3; 191/1; 220/3; 268/3; 340/1; 392/2; 475/2; 496/3; 537/1; 588/1

Query Match 9.1%; Score 456.5; DB 2; Length 674;
 Best Local Similarity 23.8%; Pred. No. 1.7e-23;
 Matches 170; Conservative 104; Mismatches 230; Indels 211; Gaps 35;

QY 141 ESHWDDDCCEIKAAECPA-GFVRPPLIIFSDVGFASYMKKSGKVPNIEKLRSCGTHS 199
 Db 108 EYKWA--GCENL--GKQIDGFTPLVILSFDGFAKEYLER--RIVKSLELIAEGVKA 161
 QY 200 PYMRPVYPTKFPNLYTLATGLYPESHGIVGNSWYDP-VFDFATHLRGKFNHRWGGQ 258
 Db 162 DRVYPSFSPKTFPNHYTMTVGLYPESHGITDNYVFDNLYPELLAMRKHEA--KEYIQAE 219
 QY 259 PLWITATKO--GVKAGTFEWSVVIPIHERRITILRWLTPDHERPSVYAFYS---EQPDF 313
 Db 220 PIW-SAYKKRLTGNRVHCLFW-----VGCYNYITGYMPD- 251
 QY 314 SGHKYGPFGPEESSYSGPTPAKRPKRVAPKRRQRPVAPPKRRRKIRHMDHYAAETR 373
 Db 252 -----VSPDYNQELPL-----KER 265
 QY 374 QDKWNTNPLREIDKIVGQMDGLKOLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNLYTNVD 433
 Db 266 IDTVNQLEEVNVIIDILMKALHDENLLECVNLVIVSDHGMQAL---NNSIEVETIVND 322
 QY 434 DITLVPGTILGRIRSKFSNNKAYDPKAIITANLTCKPDDHFPYKQLKHLPKRLHYANNRR 493
 Db 323 GLVLSKGVVARH---LNETDRSIDVAGEIRCK--IDGVKVTNTINDIPLRKHYSKRV 377
 QY 494 EDIHLVERRWHVARKPLDVYKPKSGCKFFO-----GDHGFNKNVSMOTVFVGYGPTFK 548
 Db 378 GDI--IIE-----GKP-GTSFVKSETNLGDHGYDHNNMHTVMFARGPSFL 421
 QY 549 YKTKVPPFENIELYNVMDLLGLK-PAPNNGTHGSLNHLRTNTPRTPPEVTR--PNYP 606
 Db 422 QNVTVPFQNVQYTMNLWLYLLGLEGTVDNNGTIGFFDSILKNPPIRENKNWDSMEELNFG 481
 QY 607 GIMYLSQDFDLGCTCDKVEPKNKLDELAK--RLHTKSTGEERHL-LYGRPAVLYRTRYDI 664
 Db 482 SAEVIQ-----CD-----RAEGHDLKLSLHLENCKEHLNLIYSK----- 517

QY 665 LYHTDPESYSEIFLMLTSTYTSVSKQAEVSSVDPDHLTSCVRPDVR-----VSPFSQSN 718
Db 518 --NNCFQS-YCE-----NSLIHKN-----RQDVRKGVIESLTFSSFRN 553
QY 719 CLAYKNDKQMSGFLPPY-----LSSSPEAKY---DAFLTNMV 755
Db 554 QSVFEN-----SFSVTKYSIECPKLDTKDNFTAGSEALSKLANQYKFPSSFMKSELI 609
QY 756 PMYPAPK-----RVMYFQRVLVKKYASERNGVNVISGPIFDYDYGDLHDTED 803
Db 610 SSLLSLKDETIKFVDIWWPLS-IKTDEYLKHYKLFVLSGLAVDRNLDTADDEE 663

RESULT 15
A41179
N:Alternate names: MAPK; major acidic fibroblast growth factor-stimulated phosphoprotein
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-May-1992 #sequence_revision 22-Apr-1995 #text_change 30-Apr-1999
C:Accession: A41179; A49308
R:Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 266, 16791-16795, 1991
A:Title: The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein kinase
A:Reference number: A41179; MUID:91358477
A:Accession: A41179
A:Molecule type: protein
A:Residues: 1-26;36-56;59-67;68-133;134-144;145-267;268-300 <DA>
A:Experimental source: liver
R:Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 268, 27318-27326, 1993
A:Title: The major acidic fibroblast growth factor (aFGF)-stimulated phosphoprotein from
esterase activities.
A:Reference number: A49308; MUID:94086550
A:Accession: A49308
A:Molecule type: protein
A:Residues: 27-35;X',37-58 <OD>
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBIP:141583)
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: glycoprotein; phosphoprotein; phosphotransferase
F:1-25/Domain: somatomedin B homology (fragment) <SBH>
F:36/Binding site: AMP (thr) (covalent) #status predicted

Query Match 9.1%; Score 456; DB 2; Length 300;
Best Local Similarity 18.7%; Pred. No. 6.3e-24;
Matches 150; Conservative 45; Mismatches 86; Indels 522; Gaps 14;

QY 107 RCGEVNRNEENACHCEDCLARGDCCTNYQVCKGESHVYDDDCCEIKAAECPAGFVRPPL 166
Db 2 RCFE-RTFGN-CRCDAACVELGNCCLD----- 26
QY 167 IIFSVDGFRASYMKKSGKVMPIEKLRSCGTHSPYRVPYPTKTPNLYTLATGLYPESH 226
Db 27 -----NNRPVYPTKTPNLYTLATGLYPESH 52
QY 227 GIVGNSMYPVDFATFHLRGREKFNHRWNGGOLWTATKQGVKAGTFE----- 276
Db 53 GIIDNK-----GEPILWTA-----KSGTFEWPQSDVKINGI 83
QY 277 -----SVVIPHERRILTLRLWTLPLDHPERSVYAFYSEQDFSGHKRYGPGFPSESSYVGP 331
Db 84 FPDYXVSVPFEEILAILKWLQLP----- 108
QY 332 FTPAKRPRKRVAPKRRQRPVAPPKRRKRIHRMDHYAAETRODKMTNPLREIDKIVGQL 391
Db 109 ----- 108
QY 392 MDGLKQLKLRCCVNVIFVGHGMDVTCDRTEFLSNLYTNVDDITLVPGTLGRSKFSN 451
Db 109 -----KELNLHRCNLILISDHGMEGSCSKYYSF-----DYEG 141

QY 452 NAKYDPKAIILANLTCKKPDQHFKPYLKQHLKARLHYANNRRIEDIHLIVERHWYARPL 511
Db 142 IAKSD-----RIERLTFYLDQWQALNPS 166
QY 512 DVYKKPSKCFQGDHGFDNKVNSMOTVFVGVPFTKTKVTPPENIELYNMCDLGL 571
Db 167 E--RKYCG---GGFHGSDNLFANQALFXXXXXXHSTEVDSFENIEVNLNCDLNL 220
QY 572 KPAPNNGTHSLNHLRLTNTFRPTPEEVTRPNYPGIMYLAQSDFDLGTCTDDKVEPKNKL 631
Db 221 TPAPNNGTH----- 229
QY 632 DELAKRLHTKSTEEERHLLYGRPAVLRYTRYDILYHTDFESGYSEIFLMLLWTSYTSVKQ 691
Db 230 ----- 229
QY 692 AEVSSVPDHLTSCVRPDVVRVSPFSQNCLAYKNQKMSYGFLLPPLSSSPEAKY-DAFL 750
Db 230 -----LSYGLSPPLHKGSSQVYSEALL 253
QY 751 VTNNVPMYPAFKRVWNYFQRLVKKYASERNGVNVISGPIFDYDYGDLHDTEDKIKQYVE 810
Db 254 TTNIVPMYQSQVI----- 267
QY 811 GSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSDESKWVEE 870
Db 268 -----HESLWVEE 275
QY 871 LMKMHTARVRDIEHLTSLDFFRK 893
Db 276 LLKLHTARITDVEHITGLSFYQQ 298

Search completed: July 19, 2001, 14:45:54
Job time: 152 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:44:18 ; Search time 16.91 Seconds
(without alignments)

1853.564 Million cell updates/sec

Title: US-09-483-831-69

Perfect score: 5019

Sequence: 1 MARRSFQSQIISLFFAV.....RSYPEILTKLYLHYESEI 915

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	1955.5	39.0	873	1	PC1_HUMAN	P22413 homo sapien
2	1899.5	37.8	871	1	PC1_MOUSE	P06802 mus musculus
3	410	8.2	743	1	YCR6_YEAST	P25353 saccharomyc
4	335.5	6.7	493	1	YEB6_YEAST	P39997 saccharomyc
5	238	4.7	61	1	PPD1_BOVIN	P15396 bos taurus
6	146.5	2.9	329	1	NUC1_YEAST	P08466 saccharomyc
7	123	2.5	4655	1	LRP2_HUMAN	P98164 homo sapien
8	122	2.4	1323	1	LR23_CAEEL	P24348 caenorhabdi
9	121	2.4	1888	1	YDT2_SCHPO	O14207 schizosacch
10	119.5	2.4	252	1	NUC1_CUNEE	P81203 cunninghame
11	119.5	2.4	475	1	VTNC_RABIT	P22458 oryctolagus
12	117	2.3	335	1	NUC1_SCHPO	Q10480 schizosacch
13	116.5	2.3	989	1	YD30_YEAST	P32898 saccharomyc
14	112	2.2	1394	1	TGFB_HUMAN	P22064 homo sapien
15	111.5	2.2	2396	1	NUCG_BOVIN	P38447 bos taurus
16	111	2.2	1396	1	ITAZ2_DROME	P12080 drosophila
17	111	2.2	2871	1	FBN1_HUMAN	P35555 homo sapien
18	110.5	2.2	294	1	NUCG_MOUSE	O08600 mus musculus
19	110.5	2.2	478	1	VTNC_MOUSE	P29788 mus musculus
20	110.5	2.2	2871	1	FBN1_BOVIN	P98133 bos taurus
21	110	2.2	753	1	Y705_CAEEL	O01975 caenorhabdi
22	109.5	2.2	1472	1	ATC9_YEAST	Q12697 saccharomyc
23	108.5	2.2	320	1	NUC1_SYNRA	P81204 syncephalas
24	108	2.2	1065	1	YD22_SCHPO	O13710 schizosacch
25	106	2.1	1106	1	SFC_DROME	P40798 drosophila
26	106	2.1	1178	1	YNI7_YEAST	P48231 saccharomyc
27	106	2.1	2204	1	RRPL_NDVB	P11205 newcastled
28	106	2.1	2871	1	FBN1_MOUSE	Q61554 mus musculus
29	106	2.1	3099	1	POLG_PEMVM	O56075 p genome po
30	105.5	2.1	1612	1	MTDM_PARLI	Q27746 paracentrot
31	105.5	2.1	1808	1	TENA_CHICK	P10039 gallus gall
32	104.5	2.1	2201	1	TENA_HUMAN	P24821 homo sapien
33	104.5	2.1	4289	1	TENX_HUMAN	P22105 homo sapien

RESULT 1

ID	PC1_HUMAN	STANDARD;	PRT;	873 AA.
AC	P22413; Q9Y6K3; Q9UP61;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE			
DE	PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE			
DE	(EC 3.6.1.9) (NPPASE)].			
GN	PDNP1 OR PC1 OR NPPS.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91009202; PubMed=2211644;			
RA	Buckley M.F., Loveland K.A., McKinstry W.J., Garson O.M., Goding J.W.;			
RT	"Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human			
RT	molecule, amino acid sequence, and chromosomal location.";			
RL	J. Biol. Chem. 265:17506-17511(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92246539; PubMed=1315502;			
RA	Funakoshi I., Kato H., Horie K., Yano T., Horii Y., Kobayashi H.,			
RA	Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T.,			
RA	Yamashina I.;			
RT	"Molecular cloning of cDNAs for human fibroblast nucleotide			
RT	pyrophosphatase.";			
RL	Arch. Biochem. Biophys. 295:180-187(1992).			
RN	[3]			
RP	SEQUENCE OF 93-133 FROM N.A., AND VARIANT GLN-121.			
RX	MEDLINE=99408501; PubMed=10480624;			
RA	Pizzuti A., Frittitta L., Argiolas A., Baratta R., Goldfine I.D.,			
RA	Bozzali M., Ercolino T., Scariato G., Iacoviello L., Vigneri R.,			
RA	Tassi V., Trischitta V.;			
RT	"A polymorphism (K121Q) of the human glycoprotein PC-1 gene coding			
RT	region is strongly associated with insulin resistance.";			
RL	Diabetes 48:1881-1884(1999).			
CC	-!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.			
CC	-!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES			
CC	SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED			
CC	OLIGO-NUCLEOTIDES.			
CC	-!- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.			
CC	-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.			
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER			
CC	OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE			
CC	OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.			
CC	-!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			

ALIGNMENTS

34	104	2.1	470	1	BER1_YEAST	P38934	saccharomyc
35	104	2.1	659	1	AMIA_STRPN	P18791	streptococc
36	104	2.1	700	1	KPC2_DROME	P13677	drosophila
37	104	2.1	969	1	DPOM_NEUIN	P33538	neurospora
38	103.5	2.1	297	1	NUCG_HUMAN	Q14249	homo sapien
39	103	2.1	755	1	P100_HSV7J	P52519	human herpe
40	103	2.1	1700	1	BAR3_CHITE	Q03376	chironomus
41	102.5	2.0	369	1	PF11_HUMAN	P21128	homo sapien
42	102.5	2.0	747	1	FHUA_ECOLI	P06971	escherichia
43	102.5	2.0	1426	1	EGFR_DROME	P04412	drosophila
44	102	2.0	563	1	IDS_MOUSE	Q08890	mus musculu
45	102	2.0	1018	1	FNBA_STAAU	P14738	staphylococ


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DR EMBL: X59720; CAA42318.1; -.
DR PIR: S19437; S19437.
DR PIR: S27380; S27380.
DR SGD: S0000621; YCR026C.
DR InterPro: IPR002591; -.
DR Pfam: PF01663; Phosphodiesterase 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 114 135 POTENTIAL.
SQ SEQUENCE 743 AA; 84915 MW; 23859F4BA948B0D CRC64;

Query Match      8.2%; Score 410; DB 1; Length 743;
Best Local Similarity 24.0%; Pred. No. 5.4e-22;
Matches 126; Conservative 76; Mismatches 178; Indels 146; Gaps 18;

QY 164 PPLIFSDGFRASYM-KKGSKVPNIEKLRSCG-----THSPYMRPVYPTKTFPNLYTLA 218
   | : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 168 PLTIVISLDGFHPLSKRNTPTLHDLVELKYDGMNITSPFMTIPSPFTTFPNHWTLV 227

QY 219 TGLYPESHGIVGSMYDPVDATPHLRGKFNHRWGG-----QPLWITATKQ-----GVK 270
   | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 228 TGOYPIHHGIVSNFWDPLNEEFH-----PGVLDPRIMNNNDTEPIWQVQSAFDDGDIPEK 284

QY 271 AGTFEW-----SVVIPHERILITLRLWT 294
   | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 285 AATHMPGSDVNTKYTEKQLPEHKKPIARETPTFYDFDFNAKEPLUSQKLSKTIIEYVD 344

QY 295 LPD-HERPSYIAFYSEQDSGHYKYPGPESSYSGSPPTPAKRPRKRVAPKRROERPA 353
   : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 345 MSTLNERPQLIGVVPVDAFGKHG--YPSESEY----- 377

QY 354 PPKRRRKIRHMDHYAAETQDKMTNPLRETDKIVGQMLDGLKQLKRCVNVIVFGDHG 413
   : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 378 -----YY-----EDETETLGEVDTFLKQLVESLQERNLTSTNLVIVSDHG 418

QY 414 MEDVTCD-----RTFELSNLTNVDDITLVPCTGLRISKFSNNAKYDPKA 459
   | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 419 MSDIVPSNVIIWEDLLDEKLKRDYVSH-----AYLEGPMMAISLUKDSGNI-----NE 466

QY 460 IIANLTCKPKDQHFKPKYLKQHLKRLHY--ANNRRIEDIHLVRRWHVARKPL----- 511
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 467 VYHNLKTSIDEDKYTVVNGNFKPEWFDNCKNHMAISIIWIPGAYAMKKEQLKVKAK 526

QY 512 -DYKKPDKCFQGGDHGDNKNSMOTVFGYGTFFKYTKVPPFENIELYNVWCDLLG 570
   : | | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 527 GDHKDKNEDNVFTIGSHGYDNNADMRSVFTGMGPYFP-QGYIEPFQNTIYNLLCDICG 585

QY 571 LKPAPNNGTHGSLNHLRTNFTPTMPEEVTRPNYPGIMYLOSDFD 616
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 586 VAEKDRNSNDGT--GMLMNQLREPOSSEVE-----IEDDFD 620

RESULT 4
YEB6_YEAST
ID YEB6_YEAST STANDARD; PRT; 493 AA.
AC P39997;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOPHETICAL 57.4 KDA PROTEIN IN PMP2-VAC8 INTERGENIC REGION.
GN YEL016C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Beruo A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath R., Norgren R., Oefner P., Oh C.,

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RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YCR26C.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U18530; AAB64493.1; -.
DR SGD: S0000742; YEL016C.
DR InterPro: IPR002591; -.
DR Pfam: PF01663; Phosphodiesterase 1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 57354 MW; 10B67A05C6DEDF09 CRC64;

Query Match      6.7%; Score 335.5; DB 1; Length 493;
Best Local Similarity 24.8%; Pred. No. 7.6e-17;
Matches 116; Conservative 71; Mismatches 153; Indels 127; Gaps 21;

QY 167 IIFSVDGFRASYM-KKGSKVPNIEKLRSCG-----THSPYMRPVYPTKTFPNLYTLATGL 221
   | : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 79 ILISIDGFHPLRIDAKYPTFLYLNHLRSPYDMNITATPYMIPSTFTQTFPNHWSMTGK 138

QY 222 YPESHGIVGSMYDPVDATPHLRGKFNHRWGG-----GQPLW--ITATKQGVKAGTFEW 276
   | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 139 YPIEHGIVSNIFWMDNTSSEFR---PNNLDARIWNTADPIMOLLQTESQGEYKVKATHMW 195

QY 277 ---SVV-----IPHER-----RITILRLWLTLPD-HERPSYIAFYSEQ 310
   | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 196 PGSEVYEDHGDVPRERMPFYGKFNQWKEKLDQKLAIFRYIDMPQLKDRPELVISYIPN 255

QY 311 PPSGHYKYPGPESSYSGSPPTPAKRPRKRVAPKRQERPVAPPKRRRKIRHMDHYAA 370
   | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 256 VDSYGHSGF----- 265

QY 371 ETRQDKMTNPLREIDKIVGQMLDGLKQLKRCVNVIVFGDHGMDVTCDRTEF----- 424
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 266 DLRDRKLQKLGVEVDGFFLDLIEGLQKRLNLTISNYMIVSDHGMNVDNANDGEHVYVWER 325

QY 425 -----LSNVLNVDDITLVPCTGLRISKFSNNAKYDPKAIITANLTCKKPDQ---HEKP 475
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 326 VFPADAMSAFISHLN-----EGPMVMVCLNPRDKWICOLIEAQLEKAYGEISKRHFV 381

QY 476 YLKQHLPL---KRLHYANR-----RIEDIHLLVERRMHVARKPLDYKKPSGKCFQGDH 527
   | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 382 ILKEDFDPSWKYFYDNRKRYDRVGDVIWLADYYAIVKMGDV---PIG---IMGTH 435

QY 528 GFD-NKVNMSQVTVFGYGTFFKYTKVPPFENIELYNVWCD---LLG 570
   | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 436 GYNFNNCSDMASITFGMGPMFNNEV-VPPFENIEVYNMLIKASALIG 481

RESULT 5
PPD1_BOVIN
ID PPD1_BOVIN STANDARD; PRT; 61 AA.
AC P15396;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE
DE PHOSPHODIESTERASE) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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FT	DOMAIN	2202	2244	LDL-RECEPTOR CLASS B 22.
FT	DOMAIN	2246	2288	LDL-RECEPTOR CLASS B 23.
FT	DOMAIN	2290	2331	LDL-RECEPTOR CLASS B 24.
FT	DOMAIN	2342	2383	EGF-LIKE 9.
FT	DOMAIN	2431	2476	LDL-RECEPTOR CLASS B 25.
FT	DOMAIN	2478	2517	LDL-RECEPTOR CLASS B 26.
FT	DOMAIN	2519	2561	LDL-RECEPTOR CLASS B 27.
FT	DOMAIN	2563	2603	LDL-RECEPTOR CLASS B 28.
FT	DOMAIN	2604	2646	LDL-RECEPTOR CLASS B 29.
FT	DOMAIN	2651	2693	EGF-LIKE 10.
FT	DOMAIN	2698	2738	LDL-RECEPTOR CLASS A 16.
FT	DOMAIN	2739	2777	LDL-RECEPTOR CLASS A 17.
FT	DOMAIN	2778	2819	LDL-RECEPTOR CLASS A 18.
FT	DOMAIN	2820	2861	LDL-RECEPTOR CLASS A 19.
FT	DOMAIN	2862	2901	LDL-RECEPTOR CLASS A 20.
FT	DOMAIN	2946	2945	LDL-RECEPTOR CLASS A 21.
FT	DOMAIN	2946	2990	LDL-RECEPTOR CLASS A 22.
FT	DOMAIN	3091	3029	LDL-RECEPTOR CLASS A 23.
FT	DOMAIN	3030	3070	LDL-RECEPTOR CLASS A 24.
FT	DOMAIN	3073	3110	LDL-RECEPTOR CLASS A 25.
FT	DOMAIN	3111	3151	EGF-LIKE 11.
FT	DOMAIN	3152	3192	EGF-LIKE 12.
FT	DOMAIN	3239	3280	LDL-RECEPTOR CLASS B 30.
FT	DOMAIN	3282	3331	LDL-RECEPTOR CLASS B 31.
FT	DOMAIN	3333	3375	LDL-RECEPTOR CLASS B 32.
FT	DOMAIN	3377	3418	LDL-RECEPTOR CLASS B 33.
FT	DOMAIN	3419	3459	LDL-RECEPTOR CLASS B 34.
FT	DOMAIN	3465	3509	EGF-LIKE 13.
FT	DOMAIN	3510	3550	LDL-RECEPTOR CLASS A 26.
FT	DOMAIN	3551	3591	LDL-RECEPTOR CLASS A 27.
FT	DOMAIN	3592	3632	LDL-RECEPTOR CLASS A 28.
FT	DOMAIN	3633	3673	LDL-RECEPTOR CLASS A 29.
FT	DOMAIN	3676	3716	LDL-RECEPTOR CLASS A 30.
FT	DOMAIN	3717	3756	LDL-RECEPTOR CLASS A 31.
FT	DOMAIN	3757	3795	LDL-RECEPTOR CLASS A 32.
FT	DOMAIN	3796	3834	LDL-RECEPTOR CLASS A 33.
FT	DOMAIN	3840	3880	LDL-RECEPTOR CLASS A 34.
FT	DOMAIN	3881	3922	LDL-RECEPTOR CLASS A 35.
FT	DOMAIN	3926	3964	LDL-RECEPTOR CLASS A 36.
FT	DOMAIN	3966	4006	EGF-LIKE 14.
FT	DOMAIN	4007	4048	LDL-RECEPTOR CLASS B 35.
FT	DOMAIN	4154	4195	LDL-RECEPTOR CLASS B 36.
FT	DOMAIN	4197	4239	LDL-RECEPTOR CLASS B 37.
FT	DOMAIN	4242	4282	EGF-LIKE 16.
FT	DOMAIN	4330	4368	EGF-LIKE 17.
FT	DOMAIN	4377	4411	
Query Match 2.5%; Score 123; DB 1; Length 4655;				
Best Local Similarity 16.8%; Pred. No. 3.2;				
Matches 189; Conservative 118; Mismatches 303; Indels 516; Gaps 54;				
Qy	25	CLGFTAHRIKRAEGW	-----EEGPPTVLSDSPWNTNIGSGCKGRCFELQ-----	68
Db	1200	CIGVT	-----NRCDGVFDCSDNSDEAGCP-----TRPGMCHSDEFQCEQDGIPIPNF	1247
Qy	69	---AGPPDC	-----RCNLCKSYTSCCHDFDELCLKTARGWECKT	105
Db	1248	WECDCGHPCLYSGDEHNACVPKTPCSSYFHCN	-----GNCIH-----RAMLCDR	1292
Qy	106	DR-CGEVNEENA	-----CHCSE-----DCLARGDCCTNYQVWKG-----	ESHWD-D 147
Db	1293	DNDCGDSDEKDCPTQPRPCSPWQMCGLGH-NICVNLVSVYCDGIFDCPNGTDESPLCNGN	1351	
Qy	148	DCEEIK	-----AECFAGFVRPPLIFSVDFGRASYMKKGYMPNIEK	191
Db	1352	SCSDPNGGCTHECVQEPFGAKCLCPGLF	-----LANDSKTCEIDCED	1395
Qy	192	LRSCGTHSPYMRPVY	-----PTKTF	211
Db	1396	ILGSCSOHCYNRGRFCSDTGYMLESIGRTCKVTASESILLVYASQNKIADSVTSQV	1455	
Qy	212	PNLYTLA-TGLY	-----PESHGIVGNSMYDP-----VFDATFHLR	245

Db	1456	HNISLVENGSIYVAVDFDSISGRIFWSDATQGTWSAFQNGTDRRVVDFSSIIITETIA	1515
QY	246	---GREKF-----NHR-----W--WGG 257	
Db	1516	IDWGRNLWTDYALETIEVSKIDGSHRTVLISKNLTPRGLALDPRMNEHLLFWSDWGH	1575
QY	258	QPLMITATKQG-----VKAGTFFW--SVVIPHERILTLIRMLTLPDHERPSVYAFYSEQ	310
Db	1576	HPRIERASMDGSMRTIVQDKIFWPCGLTIDYPNRLLYFM-----DSYLDYWF	1624
QY	311	PDFSGHKYGPGEPSSESSYGSFPTAKRPRKVPAPKRRQ-----ERPVA	353
Db	1625	CDYNGH-----HRRQVIASDLIIRHPYALTIFEDSVY	1656
QY	354	PPKRRRKIRHMDHYAAETRODKWTN---PLREIDKIVCOLMDGLKQLKLRRCVNVIFVG	410
Db	1657	WTDRAIRVMRANKWGHGQSVVMYNIQWPLGIVAVHPSKQPSNVNPCAFSRCSHLCLS	1716
QY	411	DHGMEDVTC-----DRTEFL-----	425
Db	1717	SGQPHFYSCVPCSGWSLSPDLLNCLRDDQPFLLITVROHIIIFGISLNPVKSNDAVPIAG	1776
QY	426	-----SNYLTNVDDITLVPGTLGRIRSKFSNNAKYDKAIIANITCKKPDQHF	473
Db	1777	IQNGLDVEFFDAEQYIYVEN-----PGEIHRVKVTGDTN-----RTVEFASISWVGPSMNL	1826
QY	474	K-PYLKQHLKRLHYANNRRIEDIHLIV-----ERRHWVARK-----PLOWYKKPS	518
Db	1827	ALDWISRN-----YSTNPTQSIIEVLTUHGDIRYKRLIANDGTALGVGPIGITVDPA	1881
QY	519	GKCFQGDHGFDNKV-----NSMTQVFVGYGPTFKYTKVPPFENIELYNVMD	567
Db	1882	RGKLYWSDQGTDSGVPAPAKIASANMDGTSVKTLFTG-----NLE--HLECV	1924
QY	568	LLGLKPAPNNGTCHSLNHLRLNTFRPTMPEEVRPNYPG-----IMYLSQDFDLGCTCDD	623
Db	1925	TLDIEE-----QKLYWAVTGRGV-----IERGNVDGDRMLVHQLSHPMGIAVHD	1970
QY	624	KVEPKNLDELNKLHKTGSTEERHLLYGRPAVLRT---RYDILVHTDFESGYSEIFL--	679
Db	1971	-----SFLYYTDEQYEVIERVDKATGANKIVLRD	1999
QY	680	---MLLWTSYTVSKQAEVSS-----VPDLHTSCVRPDRVRSFSPSQNCL	720
Db	2000	NVFNRLGLQVYHRRNAEASSNGCSNNMACQICLPVPGGLFSCA-----	2044
QY	721	AYKNDKQMSYGP-LFPYPLSSSPEAKYDAFLVTNVMVMPAFKRWVYFQRLVKKYASE	779
Db	2045	-----CATGFKLNPDRNRCSP---YNSFIVWSMLSAIRGFSLELSDRSETMYPVAGQG	2094
QY	780	RNG-----VNVISGPIFYDYGDLHDTEDKIKQY-VEGSSI-PVPTH	819
Db	2095	RNALHVDVDVSSGFIYWCDFSSSVASDNAIRRIKPDGSSLMNIVTH	2140
RESULT 8			
LT23 CAEEL			
ID	LT23 CAEEL	STANDARD;	PRT; 1323 AA.
AC	E24348;		
DT	01-MAR-1992 (Rel. 21, Created)		
DT	01-MAR-1992 (Rel. 21, Last sequence update)		
DE	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	LET-23 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112).		
GN	LET-23 OR KIN-7 OR ZK1067.1.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91080919; PubMed=1979659;		
RA	Aroian R.V., Koga M., Mendel J.E., Ohshima Y., Sternberg P.W.;		
RT	"The let-23 gene necessary for Caenorhabditis elegans vulval		

RT induction encodes a tyrosine kinase of the EGF receptor subfamily.";
RL Nature 348:693-699(1990).

[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA MEDLINE=9617760; PubMed=8604137;
RX Sakai T., Koga M., Ohshima Y.;
RT "Genomic structure and 5' regulatory regions of the let-23 gene in
the nematode *C. elegans*.";
RL J. Mol. Biol. 256:548-555(1996).

[3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Thomas K.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

[4]
RP MUTANTS.
RX MEDLINE=94147981; PubMed=8313880;
RA Aroian R.V., Les G.M., Sternberg P.W.;
RT "Mutations in the *Caenorhabditis elegans* let-23 EGFR-like gene define
elements important for cell-type specificity and function.";
RL EMBO J. 13:360-366(1994).

CC -!- FUNCTION: TYROSINE KINASE RECEPTOR REQUIRED FOR THE INDUCTION OF
C. ELEGANS VULVA. POSSIBLE RECEPTOR FOR THE INDUCTIVE SIGNAL
REQUIRED FOR VULVAL DEVELOPMENT. ACTIVATED BY LIN-3 AND ACTS BY
WAY OF LET-60 RAS. THE LIN-3/LET-23 PAIR IS A SIMPLIFIED VERSION
OF THE MAMMALIAN NEUREGULIN-ERBB NETWORK.

CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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or send an email to license@isb-sib.ch.

DR EMBL; X57767; CAA40919.1; ALT SEQ.
DR EMBL; D63426; BAA09729.1; ALT_INIT.
DR EMBL; Z70038; CAA93882.1; -
DR PIR; S13422; S13422.
DR HSSP; P11362; IFGI.

DR WormPep; ZK1067.1; CE03840.
DR InterPro; IPR000494; -
DR InterPro; IPR00719; -
DR InterPro; IPR001245; -
DR InterPro; IPR002174; -
DR Pfam; PF00757; Recep_L_domain; 2.

DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Transmembrane; Glycoprotein; Receptor; Signal.

FT SIGNAL 1 22
FT CHAIN 23 1323

FT DOMAIN 23 1323
FT DOMAIN 819 841

FT TRANSMEM 819 841
FT DOMAIN 842 1323

FT DOMAIN 885 1152
FT NP_BIND 891 899

FT BINDING 919 919
FT BINDING 1010 1010

FT ACT_SITE 91 91
FT CARBOHYD 91 91

FT CARBOHYD 169 169
FT CARBOHYD 255 255

FT CARBOHYD 376 376
FT CARBOHYD 561 561

FT CARBOHYD 655 655
FT CARBOHYD 655 655

FT CARBOHYD 746 746
FT CARBOHYD 776 776
FT VARIANT 368 368
FT VARIANT 469 469
FT VARIANT 700 700
FT VARIANT 753 753
FT VARIANT 1065 1065
FT VARIANT 1074 1074
SQ SEQUENCE 1323 AA; 150510 MW; 6B0307EE53EEFA99 CRC64;
N-LINKED (GLCNAC. . .) (POTENTIAL).
C -> Y (IN SY10).
G -> R (IN MN216).
C -> W (IN MN23).
C -> Y (IN SY11).
T -> I (IN SY16).
G -> E (IN SY17).

Query Match 2.4%; Score 122; DB 1; Length 1323;
Best Local Similarity 18.4%; Pred. No. 0.73;
Matches 149; Conservative 106; Mismatches 290; Indels 264; Gaps 43;

QY 48 SDSPWNTISGCK-----GRCFELQEAQPPDCRCDNLC-----KSTVSCC 87
DB 225 NDKCWGSDNDQRYVRSVCPKSCQCFYSNSTSSVSEC-CDSACLGCTGCHGFKNIACS 283
QY 88 -HDFELCLUKTARGWECTKDRGCEV-----RNEENACHSDEDC-----LARGDCCTNYQVY 137
DB 284 KYELDGICETCPSRKIFNHTKRLVFNPDGRYONGNHCVCPCPELLIENDVCVRH--- 340
QY 138 CKGESHV--VDD--DCEEIKAAECAGFVRPPLIIFSDGFRASYMKKSGKVPNIEKLR 193
DB 341 CSDGHHYATKDVRECEKCRSSCPK-----ICTVDGHLT-----NETLKNLEGCE 386
QY 194 SCGTHSPYMRPVYPTTFNLYTLAT-GLYPESHGVIGNSMDYDVFDAFTH-LRGREKEN 251
DB 387 QIDGH-----LIIEHAFTYQLKVLKIVSEVITVQOYFDLKFKNLIIEGKRLHN 442
QY 252 HRWGG-----QPLWITATKQGVKAGTFWVSVIPHERRIITLIRLTLDPHERPSVY 304
DB 443 VRWALAIYQCDLEELSLNSKL-ITG---AVLIMKNHRLC----- 480
QY 305 AYSQPDPSGHKYGFGFGEESYSGSFPFPAKRPKRVAPKRPQRPVAPKRRRIHR 364
DB 481 --YVSKIDWS-----IITSKGNKRPSPKLAENR----- 508
QY 365 MDHYAAETQDKMTNPLREIDKIVGQMDGLKOLKLRRCVNVIFVDGHDGMDVTCRTEF 424
DB 509 -DSKLCETEQ-----RVCDK-----NCNKGCGWKEPEDCLECKT 542
QY 425 LSNYLTNVDDITLVPGTLGRIRSKFSNNA-KYDPKAIAN-----LTCKKPDQHFQY 476
DB 543 WKSXGTCVEKC---DTKGLRNOTSMKERCSCPECETCNGELGELDLCTCRH----- 590
QY 477 LKQHLPKRLHYAN-NRIEDIHLLVRRHWVARKPL--DVYKPKSGCKCFQGDHGFQDKV 533
DB 591 -----KTLYNSDFGNRMECVH-----DCPVSHFPTQKNVCEKCHPTCYDNGCTGPDNS- 638
QY 534 NSMQTVFVGYG--PTFKYTKVPPFENIELY-----NVMC---DL----- 568
DB 639 -----LGYGCKQCKYAVK---YENDTIFCLOSGMNNVCVENLDPNYIITYDEGV 688
QY 569 -----LGLKPAFNNTHGSLNHLRLTNT-FRPTMPEEVTRPNYPYGMVYLSQDFD-- 616
DB 689 IETHCEKCSISCKTSSAGRNYYQKVCVKHVEYQPNPSEICMDQCPVNSFVPTDNT 748
QY 617 -----LGC-TCDD-----KVEPKNKLDLKNRLHYKSGSTEERHLLY 651
DB 749 VCKKCHHECDQNYHCANGOSTGCKCKNFTVFKGDIACQVSECPKPLPSNPANGECLDY 808
QY 652 GRPAVLYRTRYDILYHTDFESGYSEIFLMLL---WTSYTVSKQAEVSSVPDHLTSCVRPD 708
DB 809 DIASQRKTRMVIIGSVLF--GFVAMFLFLLVYWRQCRIGKRLKLTAEWVD-MPELTPID 865
QY 709 VRVSPFSQNC-----LAYKNDKQMSYG 731
DB 866 ASVRPNWSRICLIPSELQTKDKKLGAG 894

RESULT 9

YDT2_SCHPO
ID YDT2_SCHPO STANDARD; PRT; 1888 AA.
AC O14207;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 217.4 KDA PROTEIN C6B12.02C IN CHROMOSOME 1.
GN SPAC6B12.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Gentles S.; Churcher C.M.; Barrell B.G.; Rajandream M.A.; Wood V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; 298531; CAB1064.1;
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 697 717 POTENTIAL.
FT TRANSMEM 755 775 POTENTIAL.
FT TRANSMEM 866 886 POTENTIAL.
FT TRANSMEM 915 935 POTENTIAL.
FT TRANSMEM 977 997 POTENTIAL.
FT TRANSMEM 1033 1053 POTENTIAL.
FT TRANSMEM 1336 1356 POTENTIAL.
FT TRANSMEM 1645 1665 POTENTIAL.
FT DOMAIN 1662 1665 POLY-LEU.
SQ SEQUENCE 1888 AA; 217432 MW; 8AD3BBCE32397C29 CRC64;

Query Match 2.4%; Score 121; DB 1; Length 1888;
Best Local Similarity 17.2%; Pred. No. 1.4;
Matches 123; Conservative 101; Mismatches 223; Indels 268; Gaps 32;

QY 327 SYGSPFTPAKRPKRKVPK-----RQERPVPAPKKRRKRIHRMDHYAAETRODKMTNPL 381
DB 441 SYG-----KKAPKFLRVFARSSSHIPKMRKRQMDSKKYFSPDKESDRQV--- 486

QY 382 REIDKIVQLMDGLKQLKRCVNVIFVDHGMEDVTCRTEFLSNYLNVDITLVPGT 441
DB 487 --IDQVLSDWYSGRHELVOQ-----SHYKKPSPDSKSVGN 520

QY 442 LGRIRKFSNNAKYDPKAI IANLTCKPQDPQHPKPYLKOHLKPR-----LHVANNR 491
DB 521 I-----FSVSKKHUVINAKTAAINGLSHLQNFSEELLKRRKLFSLSFNNSVYKSK 574

QY 492 RIEDTHLVRWHVARKPLDQVY-----KKP 517
DB 575 KLRKTHTVHDKCQVAK--LDHYIRDNIELNSKEREDCYEGTLAVPQVNTETKSSRKQ 632

QY 518 SGKCFQDGHGFDKNVSMQVFGYGFYKTKVPPFENIELYNVMDLGLKPA--- 574
DB 633 KAQRIFRDD--FD-----TVFFQSSNPNYFTDVNPFWNIGWSTTENVITFRPGLSL 683

QY 575 PNNG---THGSINHLR-----TNTFRPTM-----PEVTRPNYP 606
DB 684 PNNSEFIKQOQ-LNSILQLDIVTHPEKFSYAFSCLFNIQDDVFEKTFEKLKDTFTVLENLP 742

QY 607 -----GIMVLSQDF-DLGCCTDDKVEPKKLDLNLKR 637
DB 743 YFTNSETVDLYNLSFCSAFILHSQVSMGLVNLASSFLETYALVNDVR---SSISGLN--- 797

QY 638 LHTKGSTEERHLLYGRPAVLRYTRYDILYHTDFESGYSEIFLMLLW-TSYTVSKQAEVSS 696
DB 798 -----RSQVEKIAVLFTQ-FQVYFYCEFEIGNQONINKVSWLASDLISKL--LSA 845
QY 697 VPDHLTSCVRPDRVSPFSQNCILAYKNDKQMSYGFLLPFPYLSSSPEAKYDAFLVTNNVP 756
DB 846 GQSGLLECYR-NLRQAS-----DITVIDFL-- 870
QY 757 MYPAFKRWNVYQRLV-----KKYA-----SERNGVNVIS-----GPVF 791
DB 871 ----FLESWSILNHLFHVYKKYALWEQVNSFFDLQKKLSILEMEKIVYVITLNPVF 926
QY 792 DYDYG-----LHDTEDKIKQYVEGSSIPVPHYYSITSCLDFTQPADKC 837
DB 927 QIGLNGTHSPGNSFWPLIIRVSESAFKMHKGHNKVVYRYLRTVFLRIHFLISEMRW 986
QY 838 DGPLSVSFSFI---UPHRPDNEESNSEDSESKWVEELMKMHTARVRDIEHTSLD 889
DB 987 EDVAQILFLFDFFSHRKFNLDLSEISEDPTDFDFVK-SLDRPPLN-HVTALD 1039

RESULT 10
NUCL_CUNEE STANDARD; PRT; 252 AA.
ID NUCL_CUNEE
AC P81203;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE NUCLEASE C1 (EC 3.1.30.-).
GN NUC1CE.
OS Cunninghamella echinulata var. echinulata.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
OC Cunninghamellaceae; Cunninghamella.
OX NCBI_TaxID=76406;
RN [1]
RP SEQUENCE OF 15-252 FROM N.A., AND SEQUENCE OF 1-49.
RC STRAIN=ATCC 36190;
RX MEDLINE=98417435; PubMed=9746353;
RA Ho H.-C.; Liu F.-C.; Chung J.-G.; Chen L.-Y.;
RT "Purification, characterization and complete amino acid sequence of
RT nuclease C1 from Cunninghamella echinulata var. echinulata";
RL Eur. J. Biochem. 256:112-118(1998).
CC -!- FUNCTION: THIS ENZYME HAS BOTH RNASE AND DNASE ACTIVITY.
CC -!- COFACTOR: REQUIRES MAGNESIUM OR MANGANESE FOR ACTIVITY.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
CC FAMILY.
CC
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CC
CC EMBL; AF043517; AAC78769.2;
DR InterPro: IPR001604;
DR Pfam: PF01223; Endonuclease: 1.
DR PROSITE: PS01070; NUCLEASE_NON_SPEC; 1.
KW Hydrolase; Nuclease; Endonuclease; Magnesium.
FT ACT_SITE 87 87 BY SIMILARITY.
SQ SEQUENCE 252 AA; 27498 MW; 2FA49B158AAABEC6 CRC64;

Query Match 2.4%; Score 119.5; DB 1; Length 252;
Best Local Similarity 25.0%; Pred. No. 0.13;
Matches 65; Conservative 33; Mismatches 113; Indels 49; Gaps 15;

QY 646 ERLLYGRPAVLRYTRYDILYHTDFESGYSEIFLMLLWTS--YTVSKQAEVSSVP-DHLT 702
DB 5 ESTLQGDGPG-----TARDFLERESYVISNRRDRVRSWVTGEHLTADSLKTDGVDROHSK 60

QY 703 SCVRPDYRVSPFSONCLAYKNDQMSVGFLEP--PYLSSSPKAYDAFLTNVMPYP- 759
 DB 61 FKEDPDV---PSLFRSLADYSGSGFRGHMAPAGDAVATQP-AMDQTFYLSNMSPOVQY 116
 QY 760 AFKR-VNNY---FORVLVKKYASBRGNVVISGPIF--DYDYDGLHDTEKIKQYVEGSS 813
 DB 117 GFNRHWAYLEGFCRSLTKFSD---VYFTGFLPLPTKSGDKYTYVNVLQ-----GN 168
 QY 814 IPVTHYISITSCLDFTQPADKCDGLPSVSSFLPHRPDNEESCNSSEDESKWYELMK 873
 DB 169 VAVPTHEYKVL-----VPOGDNKYAYGAFILP-----NOAID-----TKTPTLT 207
 QY 874 MHTARVRDIEHLTSLDFPRK 893
 DB 208 NFKVKLTDEKASGLTFFDK 227

RESULT 11
 VTNC_RABIT STANDARD; PRT; 475 AA.
 AC P22458;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE VITRONECTIN PRECURSOR (SERUM SPREADING FACTOR) (S-PROTEIN)
 DE (GLYCOPROTEIN 66).
 GN VTN.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
 RX MEDLINE=91065939; PubMed=1701177;
 RA Sato R., Komine Y., Inanaka T., Takano T.;
 RT "Monoclonal antibody EMR1a/212D recognizing site of deposition of
 RT extracellular lipid in atherosclerosis. Isolation and
 RT characterization of a cDNA clone for the antigen."
 RL J. Biol. Chem. 265:21232-21236(1990).
 CC -1- FUNCTION: VITRONECTIN IS A CELL ADHESION AND SPREADING FACTOR
 CC FOUND IN SERUM AND TISSUES. VITRONECTIN INTERACT WITH
 CC GLYCOSAMINOGLYCANS AND PROTEOGLYCANS. IS RECOGNIZED BY CERTAIN
 CC MEMBERS OF THE INTEGRIN FAMILY AND SERVES AS A CELL-TO-SUBSTRATE
 CC ADHESION MOLECULE. INHIBITOR OF THE MEMBRANE-DAMAGING EFFECT OF
 CC THE TERMINAL CYTOLYTIC COMPLEMENT PATHWAY.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: CONTAINS 2 HEMOPEXIN-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SOMATOMEDIN-B TYPE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M55442; AAA31258.1; -;
 DR PIR: A38340; A38340.
 DR HSSP: P45452; IPEX.
 DR InterPro: IPR000585; -;
 DR InterPro: IPR001212; -;
 DR Pfam: PF01033; Somatomedin_B; 1.
 DR Pfam: PR00045; hemopexin; 4.
 DR PRINTS: PR00022; SOMATOMEDIN.
 DR PROSITE: PS00024; HEMOPEXIN; 2.
 DR PROSITE: PS00524; SOMATOMEDIN_B; 1.
 DR Heparin-binding; Cell adhesion; Glycoprotein; Sulfatation; Signal.
 FT SIGNAL 1 19 475 VITRONECTIN.
 FT CHAIN 20 475

FT DOMAIN 20 63 SOMATOMEDIN-B LIKE.
 FT DOMAIN 150 287 HEMOPEXIN-LIKE 1.
 FT DOMAIN 288 475 HEMOPEXIN-LIKE 2.
 FT SITE 366 392 GLYCOSAMINOGLYCAN BINDING REGION.
 FT SITE 64 66 CELL ATTACHMENT SITE.
 FT MOD_RES 75 75 SULFATATION (BY SIMILARITY).
 FT MOD_RES 78 78 SULFATATION (BY SIMILARITY).
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (PROBABLE).
 SQ SEQUENCE 475 AA; 53943 MW; D5D1F31B8C2FA12D CRC64;

Query Match 2.4%; Score 119.5; DB 1; Length 475;
 Best Local Similarity 23.1%; Pred. No. 0.29;
 Matches 118; Conservative 50; Mismatches 195; Indels 147; Gaps 30;

QY 46 VLSDSPWTNISGCKRCFELQEAQPPDCRDNLCNLSYTSCHDFDELCL-KTARG---- 100
 DB 17 VLADQE-----SCDKRCTEGFNAN-RKCCDFELCSYQSCCADAEECKPQVTRGDVFT 69
 QY 101 -----WECTKDRCGEVRNEENAC-----HCSEDCLAGDCCTNQQVVKCGESHW 144
 DB 70 MPEDEYGPYDYIEQTKDNASVHAQPEPTVQGEPTLSPLDQTEGGAEPHEVPLEPEMET 129
 QY 145 VDDCEEIKAAECAGFVRPP-----LIIFSVDGPRASYMKK--GSKVM 186
 DB 130 LRPEGEDLQAGTTELGTSTASPAEEELCSGKPPDFAFTDLKNGSLFAFRGQCYVELDETA VR 189
 QY 187 PNIEKLRS--CGTHSP-----YMRPVYPTKTF---PNLYLATGL---YPE--SHGIVG 230
 DB 190 PGYPKLIQDVGWIEGPIDAAFTTRINCOGQTYLFGKQYWRFEFGILDPPDPRNISEGFGS 249
 QY 231 NSWYDPVFDATEHL-----RGREKFNHRWNGQPLWITATKO-----GVKAGFFWS 277
 DB 250 --IPDNV-DAAALPAHSYSGSERV--YFFGDKYWEYFOQOQPSOECEGSSLSAVFEH 304
 QY 278 VVIPHE---RRILTLRWLTLDPHERPSVYAFYSEQPDF-SGHKYGPFPGPESS-----Y 328
 DB 305 FAMLHRDSEDIFKLLFW-----GRPSGA---RQPFISRDWHGVPGKVDAAAGRIY 355
 QY 329 GSPFFPAKPKKVPKRVAPKRRQERVPAPPKRRKIRHMDHYAAETRODKMTNPLREIDKIV 388
 DB 356 ISGLTSPSAKKO-----KSRKRSKR---YRSRYGRRSQNS--RRLSRSI 397
 QY 389 GOLMDGLKOLKLRRCVNVIFVGDHGMEDVTCORTEFLSNLTNVDDITLVPGLGRISK 448
 DB 398 SRLWFSSESVSL-----GPYNVED-----YETS-----WLKPTSEPIQSV 433
 QY 449 --FSNNAKYDPKAITANLFCRKPDPQHFQY 476
 DB 434 YFFSGDKYR-----VNLRTQRTDVTNPPY 458

RESULT 12
 NUC1_SCHPO STANDARD; PRT; 335 AA.
 ID NUC1_SCHPO
 AC Q10480;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PROBABLE MITOCHONDRIAL NUCLEASE (EC 3.1.30.-).
 GN SPAC17C9.08.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Murphy L., McDougall R., Jones L., Simpson I., McNeil A., Harris D.,
 Barrell B.G., Rajandream M.A., Walsh S.V.;

FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 870 870 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1039 1039 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 1394 AA; 152791 MW; DFFCA81A40B2C7D1 CRC64;

Query Match 2.2%; Score 112; DB 1; Length 1394;
Best Local Similarity 23.8%; Pred. No. 4.1;
Matches 49; Conservative 17; Mismatches 48; Indels 92; Gaps 15;

QY 44 PTVLSDSPWNTSGS-----C-----KGRCFELQEAAGPPD-CR---CDNLCKSYTSCC 87
DB 678 PSTCDEQCVCNFGSVQVPCPTGEGRWGQCLVDVDECLPNVNCANGDCSNLGSYMCSC 737
QY 88 H-----DFDEL-----CLKTARGWECT-----KDR----- 108
DB 738 HKGYRTDPHKHCRDIDECQGNLVCNGCKNTGFSFRCTCGQGYQLSAAKQCEDIDEC 797
QY 109 -----GEVNEENA-----C-----HCSE--DCL-----ARGDCCT---NY 134
DB 798 QHRHLCAHQCNRTGSGFOCVCDQGYRASGLGDHCDINECLEDKSVQCRGDCINTAGSY 857
QY 135 QVCKGESHVDD--CEIKAAECP 158
DB 858 DCTCP-DGFLDDNKTCQDINECEHP 882

RESULT 15
NUGG_BOVIN STANDARD; PRT; 299 AA.
AC P38447;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G).
GN ENDOG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93342514; PubMed=7688144;
RA Cofe J., Ruiz-Carrillo A.;
RT "Primers for mitochondrial DNA replication generated by endonuclease
G.";
RL Science 261:765-765(1993).
RN [2]
RP SEQUENCE OF 49-75.
RC TISSUE=Liver, and Thymus;
RX MEDLINE=88198128; PubMed=3360771;
RA Moos M. Jr., Nguyen N.Y., Liu T.-Y.;
RT "Reproducible high yield sequencing of proteins electrophoretically
separated and transferred to an inert support.";
RL J. Biol. Chem. 263:6005-6009(1988).
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Heart;
RX MEDLINE=95175374; PubMed=7870594;
RA Gerschenson M., Houniel K.L., Low R.L.;
RT "Endonuclease G from mammalian nuclei is identical to the major
endonuclease of mitochondria.";
RL Nucleic Acids Res. 23:88-97(1995).
CC -1- FUNCTION: CLEAVES DNA AT DOUBLE-STRANDED (DG)N. (DC)N AND AT
SINGLE-STRANDED (DC)N TRACTS. IN ADDITION TO DEOXYRIBONUCLEASE
ACTIVITIES, ALSO HAS RIBONUCLEASE (RNASE) AND RNASE H ACTIVITIES.
CC CAPABLE OF GENERATING THE RNA PRIMERS REQUIRED BY DNA POLYMERASE
CC GAMMA TO INITIATE REPLICATION OF MITOCHONDRIAL DNA.
CC -1- COFACTOR: REQUIRES MANGANESE OR MAGNESIUM.

CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
FAMILY.
CC
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CC
CC EMBL; X72802; CAA51320.1; -
DR InterPro; IPR001604; -
DR Pfam; PF01223; Endonuclease; 1.
DR PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
KW Hydrolase; Nuclease; Endonuclease; Mitochondrion; Transit peptide;
KW Magnesium.
FT TRANSIT 1 48 MITOCHONDRION.
FT CHAIN 49 299 ENDONUCLEASE G.
FT ACT_SITE 143 143 BY SIMILARITY.
FT CONFLICT 172 172 H -> S (IN REF. 3; PROBABLE ERROR).
FT CONFLICT 264 264 H -> S (IN REF. 3; PROBABLE ERROR).
SQ SEQUENCE 299 AA; 32261 MW; B28FAFF56F04CFC7 CRC64;

Query Match 2.2%; Score 111.5; DB 1; Length 299;
Best Local Similarity 25.8%; Pred. No. 0.6;
Matches 32; Conservative 24; Mismatches 41; Indels 27; Gaps 6;

QY 741 SPEAKYDAFLVTNMPMPAPF-KRWVN---YFORVLVKYASERNGVNVSIGPIFDYD 796
DB 153 SQKAMDDTFYLSNVAPQVPHLNQANWNLEKYSRSLRTY----QNVYVCTGPLF----- 203
QY 797 GLHDTEDKIKQYVE-----GSSIPVPHYKYSIIISCLDFTOPADKCDGPLSVSSFIPLHR 851
DB 204 -LPRTADGKSYKVKYQVIGKNHVAVPTHFVKLI-----LEAAGGQIELRSYVMPNA 254
QY 852 PDNE 855
DB 255 PVDE 258

Search completed: July 19, 2001, 14:47:09
Job time: 171 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:43:57 ; Search time 42.51 Seconds
(without alignments)
2847.779 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSFQSCQIISLFFAV.....RSPYEILTKYLTYEISEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_16:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_unclassified:*
 - 13: sp_vertebrate:*
 - 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5019	100.0	915	4 Q13827	Q13827 homo sapien
2	4681	93.3	863	4 Q13822	Q13822 homo sapien
3	4666	93.0	863	4 Q15117	Q15117 homo sapien
4	4439.5	88.5	862	11 Q9RIE6	Q9RIE6 mus musculus
5	4306	85.8	885	11 Q64610	Q64610 rattus norv
6	2084	41.5	875	11 Q63490	Q63490 rattus norv
7	2084	41.5	875	11 P97675	P97675 rattus norv
8	2081	41.5	875	11 P70641	P70641 rattus norv
9	2057.5	41.0	876	11 Q14638	Q14638 homo sapien
10	2040.5	40.7	875	4 Q9NP23	Q9NP23 homo sapien
11	1955.5	39.0	845	4 Q9PIE6	Q9PIE6 homo sapien
12	1955.5	39.0	925	4 Q9PIE6	Q9PIE6 homo sapien
13	1151	22.9	817	14 Q90761	Q90761 fowlpox vir
14	1151	22.9	817	14 Q9J5H1	Q9J5H1 fowlpox vir
15	646.5	12.9	457	10 Q9SU82	Q9SU82 arabidopsis
16	613	12.2	479	10 Q9FS13	Q9FS13 spinacia ol
17	612	12.2	496	10 Q9SU83	Q9SU83 arabidopsis
18	611.5	12.2	479	10 Q42974	Q42974 oryza sativ
19	610	12.2	829	5 P90754	P90754 caenorhabdi

20	609	12.1	461	10 Q9SU81	Q9SU81 arabidopsis
21	539.5	10.7	485	3 Q94323	Q94323 schizosacch
22	534	10.6	251	4 Q9NQM9	Q9NQM9 homo sapien
23	526.5	10.5	257	11 Q88827	Q88827 rattus norv
24	522	10.4	429	2 Q69013	Q69013 zymomonas m
25	512	10.2	453	4 Q9Y6X5	Q9Y6X5 homo sapien
26	474.5	9.5	477	11 Q9EGC7	Q9EGC7 mus musculu
27	466.5	9.3	477	4 Q9UJA9	Q9UJA9 homo sapien
28	461	9.2	433	2 Q9PAB9	Q9PAB9 xylella fas
29	456.5	9.1	674	5 P90755	P90755 caenorhabdi
30	427	8.5	152	4 Q9H515	Q9H515 homo sapien
31	394.5	7.9	281	6 Q9TSH2	Q9TSH2 bos taurus
32	309.5	6.2	151	11 Q9QIV2	Q9QIV2 rattus norv
33	297.5	5.9	614	5 Q17540	Q17540 caenorhabdi
34	241.5	4.8	133	10 Q9SU80	Q9SU80 arabidopsis
35	238	4.7	453	5 Q22129	Q22129 caenorhabdi
36	234	4.7	45	4 Q14555	Q14555 homo sapien
37	171	3.4	385	13 Q9PTU6	Q9PTU6 paralichthy
38	170.5	3.4	44	11 Q9RID5	Q9RID5 mus musculu
39	163	3.2	360	5 Q45359	Q45359 caenorhabdi
40	158.5	3.2	1054	11 Q9JMG9	Q9JMG9 mus musculu
41	145.5	2.9	465	2 Q69954	Q69954 streptomyce
42	142	2.8	1186	14 Q55767	Q55767 chilo iride
43	135	2.7	32	6 Q9TRD2	Q9TRD2 bos taurus
44	134	2.7	1404	4 Q92954	Q92954 homo sapien
45	132	2.6	462	2 Q9Z4Z4	Q9Z4Z4 streptomyce

ALIGNMENTS

RESULT 1

Q13827 ID Q13827 PRELIMINARY; PRT; 915 AA.
AC Q13827;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
BT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE AUTOTAXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TUMOR;
RX MEDLINE=95074054; PubMed=7982964;
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,
Sobel M.E., Liotta L.A., Stracke M.L.;
RT "CDNA cloning of the human tumor motility-stimulating protein,
autotaxin, reveals a homology with phosphodiesterases.";
RL J. Biol. Chem. 269:30479-30484(1994).
DR EMBL; L35594; AAA64785.1; -;
DR InterPro; IPR001212; -;
DR InterPro; IPR001604; -;
DR InterPro; IPR002591; -;
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 915 AA; 105246 MW; 2BB6135CCD837780 CRC64;

Query Match 100.0%; Score 5019; DB 4; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSFQSCQIISLFFAVGVSICLGFTHRIKRAEGWEGPPTVLSDSPWTNISGCK 60
Db 1 MARRSFQSCQIISLFFAVGVSICLGFTHRIKRAEGWEGPPTVLSDSPWTNISGCK 60
QY 61 GRCFLEQAGPPDCRCDNLCKSVTSCCHDFELCLKTARGWECTKDRGCEVRNEENACHC 120

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Db 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHVWDDCEIEKAACPAGFVRPPLIIFSVDFGRASYMK 180
Db 121 SEDCLARGDCCTNYQVCKGESHVWDDCEIEKAACPAGFVRPPLIIFSVDFGRASYMK 180
QY 181 KGSKVPNIKLSKSCGTHSPYMRPVYPTKPNLYTLATGLYPESHGIVGNSMYDPVFA 240
Db 181 KGSKVPNIKLSKSCGTHSPYMRPVYPTKPNLYTLATGLYPESHGIVGNSMYDPVFA 240
QY 241 TFHLRGREKFNHRWGGOPPLWITATKQGVKAGTFWVSVVIPHERRILTLWLTPDHER 300
Db 241 TFHLRGREKFNHRWGGOPPLWITATKQGVKAGTFWVSVVIPHERRILTLWLTPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGFPGPESYSGSPFPAKRPKRKVAAPKRRQERVPAPPKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGFPGPESYSGSPFPAKRPKRKVAAPKRRQERVPAPPKRRR 360
QY 361 KIHRMDHYAAETRODKMTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDHGMEDVTC 420
Db 361 KIHRMDHYAAETRODKMTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDHGMEDVTC 420
QY 421 RTEFLSNLYTNVDDITLVPGTGLGRIRSKFSNNAKYDPKAIITANLTCKKPDQHFYPYLKQH 480
Db 421 RTEFLSNLYTNVDDITLVPGTGLGRIRSKFSNNAKYDPKAIITANLTCKKPDQHFYPYLKQH 480
QY 481 LPKRLHYANNRRRIEDIHLLVERHWHVARKPLDVYKPSGKCFQDGHGFDNKNVSMQTVF 540
Db 481 LPKRLHYANNRRRIEDIHLLVERHWHVARKPLDVYKPSGKCFQDGHGFDNKNVSMQTVF 540
QY 541 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKLPAPNNGTHGSLNHLRTNTFRPTMPEEV 600
Db 541 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKLPAPNNGTHGSLNHLRTNTFRPTMPEEV 600
QY 601 TRPNYPCIMYLSQDFDLCCTCDKXVEPKNDLDELNKLHRTKGTSTEEERHLLYGRPAVLRT 660
Db 601 TRPNYPCIMYLSQDFDLCCTCDKXVEPKNDLDELNKLHRTKGTSTEEERHLLYGRPAVLRT 660
QY 661 RYDILYHTDESYSYSEIFLMLLTSTYVSKOAEVSSVPDHLTSCVRPDRVYSPFSQNL 720
Db 661 RYDILYHTDESYSYSEIFLMLLTSTYVSKOAEVSSVPDHLTSCVRPDRVYSPFSQNL 720
QY 721 AYKNDKMSYGFIFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVNMYFQRLVKKYASER 780
Db 721 AYKNDKMSYGFIFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVNMYFQRLVKKYASER 780
QY 781 NGVNVISGPIFDYDGLHDETKIKQYVEGSSIPVPTHYYSIIITSCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHDETKIKQYVEGSSIPVPTHYYSIIITSCLDFTQPADKCDGP 840
QY 841 LSVSSFTLPHRPDNEESCNSDESKVVEELMKMHTARVRDIEHLTSLDFFPKTSRSYPE 900
Db 841 LSVSSFTLPHRPDNEESCNSDESKVVEELMKMHTARVRDIEHLTSLDFFPKTSRSYPE 900
QY 901 ILTKTYLHTYSEI 915
Db 901 ILTKTYLHTYSEI 915
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RESULT 2

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Q13822 ID Q13822 PRELIMINARY; PRT; 863 AA.
AC Q13822;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE AUTOTAXIN-T.
GN ATX-T.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=95074054; PubMed=7982964;
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,
RA Sobel M.E., Liotta L.A., Stracke M.L.;
RT "cDNA cloning of the human tumor motility-stimulating protein,
RT autotaxin, reveals a homology with phosphodiesterases.";
RL J. Biol. Chem. 269:30479-30484(1994).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=96158950; PubMed=8579579;
RA Lee H.Y., Murata J., Clair T., Polymeropoulos M.H., Torres R.,
RA Manrow R.E., Liotta L.A., Stracke M.L.;
RT "Cloning, chromosomal localization, and tissue expression of autotaxin
RT from human teratocarcinoma cells.";
RL Biochem. Biophys. Res. Commun. 218:714-719(1996).
DR EMBL; L46720; AA000855.1;
DR InterPro; IPR001212;
DR InterPro; IPR001604;
DR InterPro; IPR002591;
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester_1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 863 AA; 99017 MW; F960DCE51663BABC CRC64;

Query Match 93.3%; Score 4681; DB 4; Length 863;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 858; Conservative 2; Mismatches 3; Indels 52; Gaps 1;

QY 1 MARRSFQSQIISLFTFAVGYSICLGFATRAHKRAEGWEEGPTVLSDSPWNTNIGSGCK 60
Db 1 MARRSFQSQIISLFTFAVGNYNICLGFATRAHKRAEGWEEGPTVLSDSPWNTNIGSGCK 60
QY 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
Db 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHVWDDCEIEKAACPAGFVRPPLIIFSVDFGRASYMK 180
Db 121 SEDCLARGDCCTNYQVCKGESHVWDDCEIEKAACPAGFVRPPLIIFSVDFGRASYMK 180
QY 181 KGSKVPNIKLSKSCGTHSPYMRPVYPTKPNLYTLATGLYPESHGIVGNSMYDPVFA 240
Db 181 KGSKVPNIKLSKSCGTHSPYMRPVYPTKPNLYTLATGLYPESHGIVGNSMYDPVFA 240
QY 241 TFHLRGREKFNHRWGGOPPLWITATKQGVKAGTFWVSVVIPHERRILTLWLTPDHER 300
Db 241 TFHLRGREKFNHRWGGOPPLWITATKQGVKAGTFWVSVVIPHERRILTLWLTPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGFPGPESYSGSPFPAKRPKRKVAAPKRRQERVPAPPKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGFPGPE----- 324
QY 361 KIHRMDHYAAETRODKMTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDHGMEDVTC 420
Db 325 -----MTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDHGMEDVTC 368.
QY 421 RTEFLSNLYTNVDDITLVPGTGLGRIRSKFSNNAKYDPKAIITANLTCKKPDQHFYPYLKQH 480
Db 369 RTEFLSNLYTNVDDITLVPGTGLGRIRSKFSNNAKYDPKAIITANLTCKKPDQHFYPYLKQH 428
QY 481 LPKRLHYANNRRRIEDIHLLVERHWHVARKPLDVYKPSGKCFQDGHGFDNKNVSMQTVF 540
Db 429 LPKRLHYANNRRRIEDIHLLVERHWHVARKPLDVYKPSGKCFQDGHGFDNKNVSMQTVF 488
QY 541 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKLPAPNNGTHGSLNHLRTNTFRPTMPEEV 600
Db 489 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKLPAPNNGTHGSLNHLRTNTFRPTMPEEV 548
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QY 601 TRPNPGIMYLOSDFDLGCTCDDKVEPKNKLDELNKLRLHTKGTSTERRHLLYGRPAVLYRT 660
DB 549 TRPNPGIMYLOSDFDLGCTCDDKVEPKNKLDELNKLRLHTKGTSTERRHLLYGRPAVLYRT 608
QY 661 RYDILYHTDFESGYSEIFLMILMTSYTYSKQAEVSSVPDHLTSCVRPDVRSFSFSONCL 720
DB 609 RYDILYHTDFESGYSEIFLMPLMTSYTYSKQAEVSSVPDHLTSCVRPDVRSFSFSONCL 668
QY 721 AYKNDKQMSYGFLLPPYLSSSPEAKYDAFLVTNMPMPYPAFRVWNYFORVLVKKYASER 780
DB 669 AYKNDKQMSYGFLLPPYLSSSPEAKYDAFLVTNMPMPYPAFRVWNYFORVLVKKYASER 728
QY 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYIISCLDFTQPADKCDGP 840
DB 729 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYIISCLDFTQPADKCDGP 788
QY 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDFFRKTSSYPE 900
DB 789 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDFFRKTSSYPE 848
QY 901 ILTLKTYLHTYSEI 915
DB 849 ILTLKTYLHTYSEI 863

RESULT 3
ID Q15117 PRELIMINARY; PRT; 863 AA.
AC Q15117;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163899; PubMed=8586446;
RA Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J.,
RA Nakamura H., Sano K.;
RT "Molecular cloning and chromosomal assignment of the human brain-type
RT phosphodiesterase I/nucleotide pyrophosphatase gene (PDNP2).";
RL Genomics 30:380-384(1995).
DR EMBL: D45421; BAA08260.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 863 AA; 99040 MW; 318EA28BICEA7A55 CRC64;
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Query Match 93.0%; Score 4666; DB 4; Length 863;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 855; Conservative 3; Mismatches 5; Indels 52; Gaps 1;

QY 1 MARSSSFOSCOIISLTFVAVGVSICLGTFAURIKRAEGWEEGPPVTLSDSPWTNITSGCK 60
DB 1 MARSSSFOSCOIISLTFVAVGVNCLGTFAURIKRAEGWEEGPPVTLSDSPWTNITSGCK 60
QY 61 GRCFELQEPAGPPCDRCNDLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRENEENACHC 120
DB 61 GRCFELQEPAGPPCDRCNDLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRENEENACHC 120
QY 121 SEDCLARGDCCTNTQVVKCGSHWVDDCEIEKAECFAGFVRPPLIIFSVDFGRASYMK 180
DB 121 SEDCLARGDCCTNTQVVKCGSHWVDDCEIEKAECFAGFVRPPLIIFSVDFGRASYMK 180
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QY 181 KGSVMPNIEKLSCGTHSPYMRPVYPTKTPNLYTATGLYPESHGIVGNSMTDPVFDA 240
DB 181 KGSVMPNIEKLSCGTHSPYMRPVYPTKTPNLYTATGLYPESHGIVGNSMTDPVFDA 240
QY 241 TFLHURGEKENHRRWGGQPLWITATKOGVKGAGTFWSVWIPHERIILTILRWLTPDHER 300
DB 241 TFLHURGEKENHRRWGGQPLWITATKOGVKGAGTFWSVWIPHERIILTILRWLTPDHER 300
QY 301 PSYVAFYSEOPDFSGHKYGFPGPESSYGSFPFPAKRPKRKVAPKRQERVPAPPKRRR 360
DB 301 PSYVAFYSEOPDFSGHKYGFPGPE----- 324
QY 361 KIHMDHYAAETRODKMNTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTC 420
DB 325 -----MTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTC 368
QY 421 RTBFLSNYLTNVDITLVPGLTGRIRSKFSNNAKYDKAIIANLTCKKPOHFKPYLKQH 480
DB 369 RTBFLSNYLTNVDITLVPGLTGRIRSKFSNNAKYDKAIIANLTCKKPOHFKPYLKQH 428
QY 481 LPKRLHYANNRRIEDIHLVRRHWVARKPLDVYKPSGKCFQGDHGFNDKVNMSMOTVF 540
DB 429 LPKRLHYANNRRIEDIHLVRRHWVARKPLDVYKPSGKCFQGDHGFNDKVNMSMOTVF 488
QY 541 VGYGPTFKYTKVPPFENIELYNMCDLGLKPAENNGTHGSLNHLRLTNTFRPTMPEEV 600
DB 489 VGYGPTFKYTKVPPFENIELYNMCDLGLKPAENNGTHGSLNHLRLTNTFRPTMPEEV 548
QY 601 TRPNPGIMYLOSDFDLGCTCDDKVEPKNKLDELNKLRLHTKGTSTERRHLLYGRPAVLYRT 660
DB 549 TRPNPGIMYLOSDFDLGCTCDDKVEPKNKLDELNKLRLHTKGTSTERRHLLYGRPAVLYRT 608
QY 661 RYDILYHTDFESGYSEIFLMILMTSYTYSKQAEVSSVPDHLTSCVRPDVRSFSFSONCL 720
DB 609 RYDILYHTDFESGYSEIFLMPLMTSYTYSKQAEVSRVPDHLTSCVRPDVRSFSFSONCL 668
QY 721 AYKNDKQMSYGFLLPPYLSSSPEAKYDAFLVTNMPMPYPAFRVWNYFORVLVKKYASER 780
DB 669 AYKNDKQMSYGFLLPPYLSSSPEAKYDAFLVTNMPMPYPAFRVWNYFORVLVKKYASER 728
QY 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYIISCLDFTQPADKCDGP 840
DB 729 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYIISCLDFTQPADKCDGP 788
QY 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDFFRKTSSYPE 900
DB 789 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDFFRKTSSYPE 848
QY 901 ILTLKTYLHTYSEI 915
DB 849 ILTLKTYLHTYSEI 863

RESULT 4
QY 901 ILTLKTYLHTYSEI 915
DB 849 ILTLKTYLHTYSEI 863

ID Q9RIE6 PRELIMINARY; PRT; 862 AA.
AC Q9RIE6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE (EC 3.1.4.1).
GN NPPS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B/6;
RA Sano K., Piao J.-H.;
RT "Cloning and chromosomal assignment of mouse phosphodiesterase
RT I/nucleotide pyrophosphatase (PD-I alpha/autotaxin).";
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RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF123542; AAD46480.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase_1.
DR PRINTS; PR00022; SOMATOMEDIN_B.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00201; SO; 1.
KW Hydrolase.
SQ SEQUENCE 862 AA; 98918 MW; 641F8F1443B4F0B0 CRC64;
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Query Match 88.5%; Score 4439.5; DB 11; Length 862;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 806; Conservative 30; Mismatches 26; Indels 53; Gaps 2;

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QY 1 MARRSFQSCQIISLFTFAVGVSCICLGTFAHRIKRAEGWEGPPTVLSDSPTWNTSGSK 60
DB 1 MARQGCFCGSYQVISLFTFAIGVNICLGTFTASRIKRAE-WDEGPTVLSDSPTWNTSGSK 59
QY 61 GRCFELQAGPPDCRCNDLCKSYSCCHDFDELCKTARGWECTKDRGGEVNEENACHC 120
DB 60 GRCFELQAGPPDCRCNDLCKSYSCCHDFDELCKTARGWECTKDRGGEVNEENACHC 119
QY 121 SEDCLARGDCCTNYQVVKCGESHVDDCEIEKAAECPAGEVRPPLIIFSVDFRASYMK 180
DB 120 SEDCLSRGDCCTNYQVVKCGESHVDDCEIEIRVECPAGEVRPPLIIFSVDFRASYMK 179
QY 181 KGSVMPNIEKLSRSCGTHSPYMRPVYTKFPNLYTLATGLYPESHGIVGNSMDPVFDA 240
DB 180 KGSVMPNIEKLSRSCGTHSPYMRPVYTKFPNLYTLATGLYPESHGIVGNSMDPVFDA 239
QY 241 TFLRGREKFNHRWGGQPLWITATKGVKAGTFEWSVPIPHERRILTLRLWTLDPHER 300
DB 240 TFLRGREKFNHRWGGQPLWITATKGVKAGTFEWSVPIPHERRILTLRLWTLDPHER 299
QY 301 PSYAFYSEQPDFSGHKYGFPGPESSYSGSPFTPAKRPRKRVAPKRRQERVPAPPKRRR 360
DB 300 PSYAFYSEQPDFSGHKYGFPGPE----- 323
QY 361 KIURMDHYAAETQDKMTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDHGEDVTCD 420
DB 324 -----MTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDHGEDVTCD 367
QY 421 RTEFLSNLTNVDITLVPGLGRIRSKFSNNAKYDKAIITANLTKKPDQHEKPYLAKQH 480
DB 368 RTEFLSNLTNVDITLVPGLGRIRKIPNNLKYDPRAIITANLTKKPDQHEKPYLAKQH 427
QY 481 LPKRLHYANNRRIEDIHLVRRWHVARKPLDYVKPKSGKFFQGDHGFNDKNVSMQTVF 540
DB 428 LPKRLHYANNRRIEDIHLVRRWHVARKPLDYVKPKSGKFFQGDHGFNDKNVSMQTVF 487
QY 541 VYGPTFKYTKVPPFNIENLYNVCDDLGLKAPNNGTHGSLNHLRLTNTFRPTMPREV 600
DB 488 VYGPTFKYTKVPPFNIENLYNVCDDLGLKAPNNGTHGSLNHLRLTNTFRPTMPREV 547
QY 601 TRNYPGIMYLOSDFLGCTCDDKVEPKNLDELKRLTKGSTEEERHLLYGRPAVLRYT 660
DB 548 SRNYPGIMYLOSDFLGCTCDDKVKPKNLDELKRLTKGSTEEERHLLYGRPAVLRYT 607
QY 661 RYDILYHTDFESGYSEIFLMLLTSTYVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNL 720
DB 608 SYDILYHTDFESGYSEIFLPLMTSTYISKQAEVSSYPEHLTNCVRPDVRVSPFSQNL 667
QY 721 AYKNDKMSYGFLLFPYVSSSPEAKYDAFLVTNNVPMYPAKFRVMNYQFQRLVKKYASER 780
DB 668 AYKNDKMSYGFLLFPYVSSSPEAKYDAFLVTNNVPMYPAKFRVMNYQFQRLVKKYASER 727
QY 781 NGVNVISGPIFDYDGLHDTEDKIKQYVGGSSIPVPTHYIITSCLDFTQPADKCDGP 840
DB 728 NGVNVISGPIFDYDGLHDTEDKIKQYVGGSSIPVPTHYIITSCLDFTQPADKCDGP 787
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QY 841 LSVSFFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDFFPKTSRSYPE 900
DB 788 LSVSFFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTGLDLYFKTSRSYSE 847
QY 901 ILTKLYLHTYESEI 915
DB 848 ILTKLYLHTYESEI 862
RESULT 5
ID Q64610 PRELIMINARY; PRT; 885 AA.
AC Q64610;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I (EC 3.1.4.1).
GN NPH-TYPE III.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=95050605; PubMed=7961762;
RA Narita M., Goto J., Nakamura H., Sano K.;
RT "Molecular cloning, expression, and localization of a brain-specific
RT phosphodiesterase I/nucleotide pyrophosphatase (PD-I alpha) from rat
RT brain.";
RL J. Biol. Chem. 269:28235-28242(1994).
DR EMBL; D28560; BAA05910.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase_1.
DR PRINTS; PR00022; SOMATOMEDIN_B.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
KW Hydrolase.
SQ SEQUENCE 885 AA; 101309 MW; 8C5C0AFC52007973 CRC64;
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Query Match 85.8%; Score 4306; DB 11; Length 885;
Best Local Similarity 83.6%; Pred. No. 0;
Matches 792; Conservative 33; Mismatches 28; Indels 94; Gaps 6;

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QY 1 MARRSFQSCQIISLFTFAVGVSCICLGTFAHRIKRAEGWEGPPTVLSDSPTWNTSGSK 60
DB 1 MARQGCFCGSYQVISLFTFAISVNICLGTFTASRIKRAE-WDEGPTVLSDSPTWNTSGSK 59
QY 61 GRCFELQAGPPDCRCNDLCKSYSCCHDFDELCKTARGWECTKDRGGEVNEENACHC 120
DB 60 GRCFELQAGPPDCRCNDLCKSYSCCHDFDELCKTARGWECTKDRGGEVNEENACHC 119
QY 121 SEDCLARGDCCTNYQVVKCGESHVDD-----DCEIEKAAECPAGEVRPPLIIFSVDS 173
DB 120 PEDCLSRGDCCTNYQVVKCGESHVDDAARNOSSECLQV-----CP-----PPLIIFSVDS 170
QY 174 FRASYMKKSGKVMPIEKLRSCTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSM 233
DB 171 FRASYMKKSGKVMPIEKLRSCTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSM 230
QY 234 YDPVDFATFLHGRKFNHRWGGQPLWITATKGVKAGTFEWSVPIPHERRILTLRLW 293
DB 231 YDPVDFATFLHGRKFNHRWGGQPLWITATKGVKAGTFEWSVPIPHERRILTLRLW 290
QY 294 TLPDHERSVYAFYSEQPDFSGHKYGFPGPESSYSGSPFTPAKRPRKRVAPKRRQERPA 353
DB 291 SLDPNERSVYAFYSEQPDFSGHKYGFPGPE----- 321
QY 354 PPKRRRRKTHRMDHYAAETQDKMTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDHG 413
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Db 322 -----MTNPLREIDKTVQGLMDGLKQLRLHRCVNVIFVGDHG 358
Qy 414 MEDVTCDRTEFLSNLTNNVDDITLVPGLTGRIRSKFSNNAKYDPKAIANLTKCKPDQHF 473
Db 359 MEDVTCDRTEFLSNLTNNVDDITLVPGLTGRIRAKSINNSKYDPKTIANLTKCKPDQHF 418
Qy 474 KPYLKHPLKRLHYANNRRIEDHLLVERHWHVAPLVDYKPKSGCKFFQGDHGDKNV 533
Db 419 KPYMKOHLPLKRLHYANNRRIEDHLLVDRWHVAPLVDYKPKSGCKFFQGDHGDKNV 478
Qy 534 NSMQVFFVGYGTFKYKTKVPPFENIELYNVMDLLGLKLPAPNNGTHGSLNHLRLTNTER 593
Db 479 NSMQVFFVGYGTFKYKTKVPPFENIELYNVMDLLGLKLPAPNNGTHGSLNHLRLTNTER 538
Qy 594 PMPPEVTRPNYPGIMYLGSDFDLGTCDCKDVPKPKLDELNKLRLTKGSTE----- 645
Db 539 PMPPEVTRPNYPGIMYLGSEFDLGTCDCKDVPKPKLDELNKLRLTKGSTEATGKFERG 598
Qy 646 -----ERHLLYGRPAVLRYRTYDILYHTDFESGYSEIFLMLLWTSYTV 688
Db 599 SKHENKNLINGSVEPRKRLHYGRPAVLRYRTYDILYHTDFESGYSEIFLMLLWTSYTV 658
Qy 689 SKQAEVSSVPDHLTSCVRDVRVSPFSONCLAYKNDKQMSYGFLLPPYLSSSPEAKYDA 748
Db 659 SKQAEVSSIPHLTNCVRDVRVSPFSONCLAYKNDKQMSYGFLLPPYLSSSPEAKYDA 718
Qy 749 FLVTNNVPMYPAPKRVNNYFORVLKVKYASERNGVNVISGPIFDYDYGHLHDTEDKIKQY 808
Db 719 FLVTNNVPMYPAPKRVNNYFORVLKVKYASERNGVNVISGPIFDYDYGHLHDTEDKIKQY 778
Qy 809 VEGSSIPVTHYYSITSLDTPQADKCDGPLSVSSFFILPHRPDNEESCNSSEDESKWV 868
Db 779 VEGSSIPVTHYYSITSLDTPQADKCDGPLSVSSFFILPHRPDNEESCNSSEDESKWV 838
Qy 869 BELMKMHTARVDRDIEHLTSLDFRKTSSRYPETLLTKLYLHYEISEI 915
Db 839 BELMKMHTARVDRDIEHLTGLDFRKTSSRYSIELLTKLYLHYEISEI 885

RESULT 6
ID Q63490 PRELIMINARY; PRT; 875 AA.
AC Q63490:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE RB13-6 ANTIGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAQUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=9524775; PubMed=7730366;
RA Dessler H., Lottspeich F., Rajewsky M.F.;
RT "Affinity purification and cDNA cloning of rat neural differentiation
RT and tumor cell surface antigen gp130rb13-6 reveals relationship to
human and murine PC-1".
RL J. Biol. Chem. 270:9849-9855(1995).
DR EMBL; Z47987; CAA88029.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester_1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 875 AA; 99087 MW; 9BA9FBFEF82DFBA6 CRC64;
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Query Match 41.5%; Score 2084; DB 11; Length 875;

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Best Local Similarity 43.5%; Pred. No. 9.6e-162;
Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;

Qy 57 GSCKGRCFEIQEAGPPDCRDNLCYSYSCCHDFDELCLKTARGWECKTDRGCEVRNEN 116
Db 53 GSCKRKKCFDSHRRGLEGCRCDSGCTDRGDCWDFEDTCVKSTQIWCNSFRGETRLEAA 112
Qy 117 ACHSBCDLARGDCCTNYQVYCKGESHVWDDCEBIKAAECAPAGVRPLIIFSVDGPR 176
Db 113 LCSCADCLQKDKCTDYKAYCQGEVPMWTACASSQBPQCEGDPQPVILFSMDGPR 172
Qy 177 SYMKGSKVMENIEKLRSCGTHSPYMRPVYTKTPPNLYTLATGLYPESHGIVGNSWDP 236
Db 173 EYLQWTSLLEINIKLCTGHSKTYMRAMYPTKTPPNYITIVTGLYPESHGIDNNWYDV 232
Qy 237 VFDATFHLRGKEFHRHWMGQPLWITATKQGVKAGTEFF-----SV 278
Db 233 YLNKNFSLSSVEKSNPAWMSGQIWLTAHYQGLKAAASYWLGSDVAVNGSPFNIRYNSN 292
Qy 279 VIPHERILTLRLWTLTPDHERPSVYAFYSEQDFSGHKYGFPGPEESSYSGSPFPAKRP 338
Db 293 SVPYESRATLLOWDLPLKAERPSEFYTIYVEEPDSAGHKGSPV-----SAG 338
Qy 339 KRKYAPRRQERPYPAPKRRKRIHRMDHYAAETQRDKMTNPLREIDKIVGOLMDGLKQL 398
Db 339 -----VIRALQVLDDAFGLMEGLKQR 360
Qy 399 KLRCVNVIFVGDHGMEDVTCDRTEFLSNLTNNVDDITLVPGLTGRIRSK-----FSNN 452
Db 361 NLHNCVNIIVLADHGMDOOTSCDRVEYMTDYFPEI-NFYMQGPAPRIETRNIPQDFFTFN 419
Qy 453 AKYDPKAIANLTKCKPDQHFKPKYLKQHLKRLHYANNRRIEDHLLVERHWHVARKPLD 512
Db 420 S-----EETVRDLSCRKSDQHFEPVLTPLDKRLHYAKNVRDKVHLWMDVQWLAYR---- 471
Qy 513 VYKPKSGCKFFQGDHGDKNVNSMQTVFVGYPGTFKYKTKVPPENIELYNVMDLLGLK 572
Db 472 --NKGSSNC-EGGTHGYNNEFKSMEATFLAHGSPSFKEKTVIEPFENIEVYLLCDLLHIQ 528
Qy 573 PAPNNGTHGSLNHLRLTNTERPTMPERVTRPNYPGIMYLGSDFDLGTCDCKDVPKPKLD 632
Db 529 PAPNNGSHGSLNHLKAPFYQPSHAELSKSAGCGFTPLPKDSLNCSC-LALQTSQGE 587
Qy 633 ELNKLRLHTKG-----STEERHLLYGRPAVLRYTR-YDILYHTDFESGYSEIFLMLLWTSY 687
Db 588 QVNQRLNLGSEVSATEKTNLPFGRPVIOKNKDCLLYHREYVSGFGKAMPWMSY 647
Qy 688 VSKQAEVSSVPDHLTSCVRDVRVSPFSONCLAYKNDKQMSYGFLLPPYLSSSPEAKYD 747
Db 648 VPKPGDTSSLPPTVPDCLRADVRVDPSESQKCSFYLADQNTDGHGLYPPAIKGNESQYD 707
Qy 748 AFLVTNNVPMYPAPKRVNNYFORVLKVKYASERNGVNVISGPIFDYDYGHLHDTEDKIKQ 807
Db 708 ALITSNLVPYKPKKWDVFKVLLIKYAIERNGVNVVSGPIFDYNDGHGDPADETIN 767
Qy 808 YVEGSSIPVTHYYSITSLDTPQADKCDGPLSVSSFFILPHRPDNEESCNSSEDESKW 867
Db 768 VVAGTDVPVTHYFVVLTSCKNKTHTPDSCPGWLDVLPFVVPVPHRPTNVESCPENKAEDLW 827
Qy 868 VEELMKMHTARVDRDIEHLTSLDFRKTSSRYPETLLTKLYLHYEISEI 915
Db 828 VEERFKAHARVDRVDELLTGLDFYQKTPQVSEILQLTKLYLPTETII 875

RESULT 7
P97676
ID P97676 PRELIMINARY; PRT; 875 AA.
AC P97676;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE.
OS Rattus norvegicus (Rat).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250927; PubMed=9096610;
RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.,
RA Maurice M.;
RT "Biochemical and molecular identification of distinct forms of
RT alkaline phosphodiesterase I expressed on the apical and basolateral
RT plasma membrane surfaces of rat hepatocytes.";
RL Hepatology 25:995-1002(1997).
DR EMBL; U78788; AAB61536.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester_1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00201; SO; 1.
SQ SEQUENCE 875 AA; 99071 MW; 4205F263E8A9333EA CRC64;

Query Match 41.5%; Score 2084; DB 11; Length 875;
Best Local Similarity 43.5%; Pred. No. 9.6e-162;
Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;

QY 57 GSKGRCFELQEAQPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDRGCEVRNEEN 116
Db 53 GSKRKKCFDSSHRGLEGRCDSCGCTDRGCCDFEDTCVKSTQIWTCSNFRGCTRELEA 112
QY 117 ACHSEDCIARGDCCCTNYQVCKGESHWDDCEIEKAAECAPAGVRPPLIIFSVGDFRA 176
Db 113 LCSCADCLQKDCCTDYKAVCGEVPWVTEACASSQEQPCPEGDPQPVILFSDMGFRA 172
QY 177 SYMKGSKVMPNIEKLSGTHSPYMPVPTKPNLYTLATGLYPESHGIVGNSMDYD 236
Db 173 EYLQWTSTLLPNINKLTCGLHSKYMRYEPTKPNHTYITVGLYPESHGIIDNNYDV 232
QY 237 VFDATPHLRGKFNHRWGWQPLWITATKQGVKAGTEFW-----SV 278
Db 233 YLNKNFSLSSVEKSNPAWSSQIWLAMYQGLKAAASYHWPGSVDVAVNGSPFIYRNSN 292
QY 279 VIPHERILTLRLWLPDHERPSVYAFYSEQDFSGHKYGFPGPEESYSGPFTPAKRP 338
Db 293 SVPYESRIATLLQWLDLPKAERPSFTYIYVEEDSAGHSGPV-----SAG 338
QY 339 KRKVAPRRQERPVA PKPKRRKTHRMHYAAETRQDKWNTPLREIDKIVGLMDGLKQL 398
Db 339 -----VIKALQLVDDAFGIMLMEGLKOR 360
QY 399 KLRCNVNIVFGDHGMEDVTGDRTEFLSNLYTNVDDITLVPCTGLGRISK-----FSNN 452
Db 361 NLHNCVNIIVLADHGMDSCTDRVEYWDYYPEI-NFYMYOGAPAPRIKTRNIPQDFFTFN 419
QY 453 AKYDPKAIANLCKPDQHPKPYLKHLPRRLHYANNRRIEDHLLVERHWVHARKPLD 512
Db 420 S-----EIVRDLSCRSKDQHFKPYLPDLPRRLHYAKNVRIDKVKHLMDRWQLAYR---- 471
QY 513 VYKPKSKCFQGDHGFNDKNVSNMOTVFVGYGPTFKYKTKVPPRENIELYNNVMDCLGLK 572
Db 472 --NKGSSNC--EGGTHGYNNEFKSMEALFLAHGSPFKEVTIPEPNIIEYVNLCDLLHIQ 528
QY 573 PANNPHTGSLNHLRLTNTFRPTMPEEVTNRPNYPMYQLSQDFDLGCTCDKQVPEKNKLD 632
Db 529 PANNPHTGSLNHLRLKAPFYOPSHAEELSKSAGCGFTTLPKDSLNCSC-LALQTSQGE 587
QY 633 ELNKLRTKG-----STERHLLYGRPAVLYRTR-YDILYHDFESGYSEIFLMLLWTSYT 687
Db 588 QVNQRLNLSGGEVATEKTNLFFGRPRVYIQNKDKHLLYHREYVSGFGKAMKMPWSSYT 647
QY 688 VSKQAEVSSVPDHLTSCVRPDVRYSPFSQNCCLAYKNDQMSYGLFPYLLSSSPKAYD 747
Db 648 VPKGDTSSLPPTVPDCLADRVVRDPSSESQKSCSYFLADQNIDHGFLYPPATKGNSESQYD 707
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QY 748 AFLVTNNWPMYPAFKRWNYFORVLVKKYASERNGVNVISGPIFYDYDGLHPTEDIKIQ 807
Db 708 ALITSNLWPMYKEFKKMDYFHKVLLIKYAIERNGVNVYSGPIFYDYGDFDPADEITN 767
QY 808 YVEGSSIPVTHYSIITSCLDFTQPADKCDGPLSVSSFLPHRPNESCSSEDESKW 867
Db 768 YVAGTDVPTVTHYFVVLTSCKNKTHTPDCPGWLDVLPFVPHRPTNVESCPENKAEDLW 827
QY 868 VVELMKMHTARVDIEHLTSLDFFRKTSSYPBILTKLYLTHYSEI 915
Db 828 VEERFAHARVDVDELLIGLDFYQEQTPQVSEILQLKTYLPTFTFII 875

RESULT 8
P97675 PRELIMINARY; PRT; 875 AA.
AC P97675;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=97250927; PubMed=9096610;
RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.,
RA Maurice M.;
RT "Biochemical and molecular identification of distinct forms of
RT alkaline phosphodiesterase I expressed on the apical and basolateral
RT plasma membrane surfaces of rat hepatocytes.";
RL Hepatology 25:995-1002(1997).
DR EMBL; U78787; AAB61535.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester_1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 875 AA; 99166 MW; 8FEB9A4821730377 CRC64;

Query Match 41.5%; Score 2081; DB 11; Length 875;
Best Local Similarity 43.5%; Pred. No. 1.7e-161;
Matches 386; Conservative 159; Mismatches 249; Indels 94; Gaps 11;

QY 57 GSKGRCFELQEAQPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDRGCEVRNEEN 116
Db 53 GSKRKKCFDSSHRGLEGRCDSCGCTDRGCCDFEDTCVKSTQIWTCSNFRGCTRELEA 112
QY 117 ACHSEDCIARGDCCCTNYQVCKGESHWDDCEIEKAAECAPAGVRPPLIIFSVGDFRA 176
Db 113 LCSCADCLQKDCCTDYKAVCGEVPWVTEACASSQEQPCPEGDPQPVILFSDMGFRA 172
QY 177 SYMKGSKVMPNIEKLSGTHSPYMPVPTKPNLYTLATGLYPESHGIVGNSMDYD 236
Db 173 EYLQWTSTLLPNINKLTCGLHSKYMRYEPTKPNHTYITVGLYPESHGIIDNNYDV 232
QY 237 VFDATPHLRGKFNHRWGWQPLWITATKQGVKAGTEFW-----SV 278
Db 233 YLNKNFSLSSVEKSNPAWSSQIWLAMYQGLKAAASYHWPGSVDVAVNGSPFIYRNSN 292
QY 279 VIPHERILTLRLWLPDHERPSVYAFYSEQDFSGHKYGFPGPEESYSGPFTPAKRP 338
Db 293 SVPYESRIATLLQWLDLPKAERPSFTYIYVEEDSAGHSGPV-----SAG 338
QY 339 KRKVAPRRQERPVA PKPKRRKTHRMHYAAETRQDKWNTPLREIDKIVGLMDGLKQL 398
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[illegible]

Db	372	DHGMDDQYCNKMSYMTDYFPRIFFYMYEGPAPRIIR---AHNIPDHFDFSNSEIEIVRNLS	428
Qy	466	CKKPDQHFKPYLQHLPKRLHYANNRRIEDIHLVVERRHVHARKPDVDYKKPSGCKFFOG	525
Db	429	CRFPDQHFKEPYLPDLPKRLHYAKNVRIDKVLHFDVQDW-----LAVRSKSNVNC-GGG	481
Qy	526	DHGFNDKNSMOTVFGYGYGTFYKYTKVPPFENIELYVNCMDLLGLUKPAPNNGTHGSLNH	585
Db	482	NHGYNNEFRSMEAIFLAHGPSFEKTEVEYFENIYVNLMDLLRIQAPNNGTHGSLNH	541
Qy	586	LLRTNTRFPTMPVEVTRPNYPGIMYLGSDFDLCTCDKDVPEKPKLDLNLKRLHYK----	641
Db	542	LLKVPFEPESHABEVSKFSVCGFANPLPTESLDFCF-PHLQNSTOLEYQVOMLNLQTEBI	600
Qy	642	GSYTEERHLLGRAVLYR-TRYDILVHTDESIGSEYELFLLMLLWTSTVYSKQAEVSSVPDH	700
Db	601	TATVKNVLPGRPRVLOKQNVHDCHLLVHREVSGFGKAMRPMWSSITVQLGDTSPLPPT	660
Qy	701	LTSVRPDRVRSFSSQNCILAYKNDKQMSYGFLEPPPYLSSSPEAKYDAFLVTNMVPMYA	760
Db	661	VPDCLRADVRPPSESQKCFYLADKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEE	720
Qy	761	FKRWNTFQRYLVKKYASERGNVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHY	820
Db	721	FRKMWDYFVSLTIKHATERGNVNVSGPIFDYNYDGHFDAPDEIKHLANTDVPITPHY	780
Qy	821	YSIITSCLDFTQPADKCDGPLSVSSFTLPHRPNEBSCNSEDSEKWEELMKMHTHARV	880
Db	781	FVLTSCNKSHTPENCPCGWLDDVLPFIIPHRPTNVESCEPGKEALUWBERFHTAHARV	840
Qy	881	DIEHLTSLDFRFTSRSPBEILTKTYLHTYSESI	915
Db	841	DVELLTGLDFYQDKVQVPSSEILQIKYLPFTETI	875

RESULT 11

Q9NPZ3 ID Q9NPZ3 PRELIMINARY; PRT; 845 AA.

AC Q9NPZ3;

DR 01-OCT-2000 (T=EMBLrel. 15, Created)

DT 01-OCT-2000 (T=EMBLrel. 15, Last sequence update)

DI 01-MAR-2001 (T=EMBLrel. 16, Last annotation update)

DE DJ131F15.2 (PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE 1 (HOMOLOGOUS TO MOUSE LY-41 ANTIGEN) (PCL, NPFS)) (FRAGMENT). PDPN1.

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

ON [1]

RN SEQUENCE FROM N.A.

RP Peck A.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL117378; CAB99365.1; -

DR InterPro; IPR001212; -

DR InterPro; IPR001604; -

DR InterPro; IPR002591; -

DR Pfam; PF01033; Somatomedin_B; 2.

DR Pfam; PF01663; Phosphodiesterase; 1.

DR PRINTS; PR00022; SOMATOMEDINB.

DR PROSITE; PS00524; SOMATOMEDIN_B; 2.

DR SMART; SM00477; NUC; 1.

FT NON_TER 1

SQ SEQUENCE 845 AA; 96844 MW; C2DD58248BDAC52E CRC64;

Query Match 39.0%; Score 1955.5; DB 4; Length 845;

Best Local Similarity 42.2%; Pred. No. 3e-151;

Matches 370; Conservative 150; Mismatches 252; Indels 115; Gaps

Qy	58	SKCRGCFELQFAGPPDCRCNCLCKSYTSCCHDFDELCTARTGWECTKRCQVRNEENA	117
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Db 27 SCKGRCFE-RTFG--NCRDAAACVELGNCCLDYQETCIEPHEIHWTCNKFRCGEKRLTRSL 83
Qy 118 CHCEDCLARGDCCNYQVVGCGESHWVDDCEIEKAAECFAGVRRPPLIIFSVGDFRAS 177
Db 84 CACSDCKDKGDCINYSVCGEGESWVEPCEINPEQCPAGFETPTLLFLSLDGFRAE 143
Qy 178 YMKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPV 237
Db 144 YLHTWGLLPVLSKUKCCGTYTKNMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPV 203
Qy 238 FDATEHLRGREKFNHRWGGQPLWITATKQGVKAGTFFW-----SVV 279
Db 204 MNASFSLKSEKFNPEWYKGEPIWTAKYQGLKSGTFFWPGSDVEINGFPDIYKMYNGS 263
Qy 280 IPHERRIITLRLWTLDPHERPSVAFYSQDPFSGHKYGPFGPESSYGSPTPAKRPK 339
Db 264 VPFEERILAVLQWLQPKDERPHEFTYLYLEPDSGSHSGYGSVSE----- 308
Qy 340 RYVAPKRQERPVAPPKRRRKIRHMDHYAAETQDKMTNPLREIDKIYQGLMDGLKOLK 399
Db 309 -----VIRALQRVGDMGMLDGLKELN 411
Qy 400 LRRCVNIVFVGDHGMEDVTCDRTEFLSNLYTNVDDITLVPGLGRIR-----SKFSNNAK 454
Db 332 LHRCLNLILSDHGMEOGCKKIYLYLKVGLDVKNIKYIGPAARLRPSDVPDKIYS--- 388
Qy 455 YDKAIIANLCKKPKDQHFQKPKLQKHLPRKLRHYANNRRIEDIHLVRRHWARKPLDVI 514
Db 389 FNYEGIARNLSCREPNQHFQKPKLQKHLPRKLRHYANNRRIEDIHLVRRHWARKPLDVI 446
Qy 515 KPSKCKCFQDGHGDNKVNNSQTVGVGPTFKYKTKYKPPENIBELYNVWCDLLGLKPA 574
Db 447 RKYCG----SGFHGSDNVFSNNQALFVGYPGPKHGIEADTFENIEVYVNLMDCLLNLTPA 502
Qy 575 PNNGTHGSLNHLRTNTREPTPEEVTRENYPCIMYLSQDF-----DLGCTCDKVEPK 628
Db 503 PNNGTHGSLNHLKNPVYTPKPKPEV-----HP---LVQCPFTNRPNRDLGSCNPSILP- 554
Qy 629 NKLDENLRLHTKGTSTEE--RH--LLYGRPAVLYR--TRYDIILYHTDFESGYSIFLMLLW 683
Db 555 --IEDFQFQNLTVAEKIIKHETLPYGRVLORENTICLLSOHQFMSGYSQDILMPLW 612
Qy 684 TSYVTSKQAEVSSVDHDTSCVDPDVSPSPSONCLAYKNQKMSQFGLFPPLYSSEPE 743
Db 613 TSYTVDRNDSFST--EDFSNCLYQDFRIPLSVPHKCSFYKNNTKVSYGFLSPQLNKNSS 670
Qy 744 AKY-DAEVLTVNMPVPAFKRWNYFORVLVKKYASERNVNVISGPIEDYDYGDLHDTE 802
Db 671 GIYSEALLTINVPWYQSFQVIRWFYHDTLLRKRYAERNVNVSGPVDFDYDGRCDSL 730
Qy 803 DKIKQ---YVGESSIPVTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESC 859
Db 731 ENLRQKRRVIRNQELIETHFVILTCKDTSQTPHLEN-LDTLAFILPHRTDNSESCV 789
Qy 860 SSEDSEKWEELMKHMTARVDIEHTLSLDFFPKYSRSYPEILTKLYLHTYSE 914
Db 790 HGKHDSSWEELMLHRRARITDVEHITGLSFYQORKEPVSIDILKTLKTLPTFSQE 844

RESULT 12
Q9P1P6
ID Q9P1P6 PRELIMINARY; PRT; 925 AA.
AC Q9P1P6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PNP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Bozzali M., Pizutti A., Trischitta E.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110304; AAF36094.1; -
DR EMBL; AF110280; AAF36094.1; JOINED.
DR EMBL; AF110281; AAF36094.1; JOINED.
DR EMBL; AF110283; AAF36094.1; JOINED.
DR EMBL; AF110284; AAF36094.1; JOINED.
DR EMBL; AF110285; AAF36094.1; JOINED.
DR EMBL; AF110286; AAF36094.1; JOINED.
DR EMBL; AF110287; AAF36094.1; JOINED.
DR EMBL; AF110288; AAF36094.1; JOINED.
DR EMBL; AF110289; AAF36094.1; JOINED.
DR EMBL; AF110290; AAF36094.1; JOINED.
DR EMBL; AF110291; AAF36094.1; JOINED.
DR EMBL; AF110292; AAF36094.1; JOINED.
DR EMBL; AF110293; AAF36094.1; JOINED.
DR EMBL; AF110294; AAF36094.1; JOINED.
DR EMBL; AF110295; AAF36094.1; JOINED.
DR EMBL; AF110296; AAF36094.1; JOINED.
DR EMBL; AF110297; AAF36094.1; JOINED.
DR EMBL; AF110298; AAF36094.1; JOINED.
DR EMBL; AF110299; AAF36094.1; JOINED.
DR EMBL; AF110300; AAF36094.1; JOINED.
DR EMBL; AF110301; AAF36094.1; JOINED.
DR EMBL; AF110302; AAF36094.1; JOINED.
DR EMBL; AF110303; AAF36094.1; JOINED.
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 925 AA; 104924 MW; 0ECAA063801CAFEB CRC64;

Query Match 39.0%; Score 1955.5; DB 4; Length 925;
Best Local Similarity 42.2%; Pred. No. 3,4e-151;
Matches 378; Conservative 150; Mismatches 252; Indels 115; Gaps 19;

Qy 58 SCKGRCFEAGPDCRDNLCCKSYTSCCHDFDELCLKTARGWECTKDRGCEVNRNEA 117
Db 107 SCKGRCFE-RTFG--NCRDAAACVELGNCCLDYQETCIEPHEIHWTCNKFRCGEKRLTRSL 163
Qy 118 CHCEDCLARGDCCNYQVVGCGESHWVDDCEIEKAAECFAGVRRPPLIIFSVGDFRAS 177
Db 164 CACSDCKDKGDCINYSVCGEGESWVEPCEINPEQCPAGFETPTLLFLSLDGFRAE 223
Qy 178 YMKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPV 237
Db 224 YLHTWGLLPVLSKUKCCGTYTKNMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPV 283
Qy 238 FDATEHLRGREKFNHRWGGQPLWITATKQGVKAGTFFW-----SVV 279
Db 284 MNASFSLKSEKFNPEWYKGEPIWTAKYQGLKSGTFFWPGSDVEINGFPDIYKMYNGS 343
Qy 280 IPHERRIITLRLWTLDPHERPSVAFYSQDPFSGHKYGPFGPESSYGSPTPAKRPK 339
Db 344 VPFEERILAVLQWLQPKDERPHEFTYLYLEPDSGSHSGYGSVSE----- 388
Qy 340 RYVAPKRQERPVAPPKRRRKIRHMDHYAAETQDKMTNPLREIDKIYQGLMDGLKOLK 399
Db 389 -----VIRALQRVGDMGMLDGLKELN 411
Qy 400 LRRCVNIVFVGDHGMEDVTCDRTEFLSNLYTNVDDITLVPGLGRIR-----SKFSNNAK 454
Db 412 LHRCLNLILSDHGMEOGCKKIYLYLKVGLDVKNIKYIGPAARLRPSDVPDKIYS--- 468
Qy 455 YDKAIIANLCKKPKDQHFQKPKLQKHLPRKLRHYANNRRIEDIHLVRRHWARKPLDVI 514
Db 469 FNYEGIARNLSCREPNQHFQKPKLQKHLPRKLRHYANNRRIEDIHLVRRHWARKPLDVI 526

	QY	515	KPSGKCFGGDGHFNKNVSMQTFFVGYPFTFKYTKVPFPFENIELYNVMCDLLGLKPA	574
	Dd	527	RKYC-----SGFHGSNDNVFSNMQLFVGYPGFKGHTEADTFENIEVINLMDCLLNTPA	582
	QY	575	PNNCTHGSNLHLRTNFRPTMPBEVTNPYPGTWYLQSDF-----DLGCCTDDKVPEPK	628
	Dd	583	PNNCTHGSNLHLKPNYYTTPKHKEV-----HP-----LVQCPTNRPRDNLGCSNPILP-	634
	QY	629	NKLDELAKRLHTKTSTEE--RH---LLYGRPAVLVR-TRYDILYTHDPESGYSEIFMLLW	683
	Dd	635	--IEDFOFOTQNLTVAREKKIHKETLPVGRPVLOKENTICLLSHOHFMMSGYSODILMPLW	692
	QY	684	TSYTVSKOAEVSSPYVDHLTSCVRPDVRSPSFSONCLAYKNDKOMXSGFLPPFYLSSTE	743
	Dd	693	TSYTVDNRDSFST--EDFSNCLYQDRIPLSVPVKHSFYKNTKVSYGFLSPPOLNKSS	750
	QY	744	AKY-DALVLTNVWPYAPAFKRWNVFORVLVKKYASERNGVNVISGPFIYDYDGLHDTE	802
	Dd	751	GIYSEALLTTINIVPMYOSFQVIWRIFYFDTLRKYAERNGVNYVSGPFVDFDYDGRCDSL	810
	QY	803	DKIKQ---YYEGSGIPYPTHYSISITSLDFTOPADCKDGPLSVSSFILPHRPDNEESC	859
	Dd	811	ENLRQRVRVIRNQELLIPTHFIVLTSCKDTSQTPLHCEN-LDIATFILPARTNSESCV	869
	QY	860	SSEDESKWEELMKMHARTVARDIEHLTSLDFFRKTSRSYPEILTKTYLHYESE	914
	Dd	870	HGXKDSSWEELMLHRARITDVHEITGLSFYQQRKPEVSDILKLTPLTFSEQE	924
	RESULT	13		
	ID	O90761	PRELIMINARY; PRT; 817 AA.	
	AC	O90761;		
	DT	01-NOV-1998 (TREMBLrel. 08, Created)		
	DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
	DE	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
	DT	ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5' -		
	DE	NUCLEOTIDE PHOSPHODIESTERASE).		
	GN	PCI.		
	OS	Fowlpox virus.		
	OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;		
	OC	Avipoxvirus.		
	NCBI_TaxID=10261;			
	RN	[1]		
	PC	SEQUENCE FROM N.A.		
	RC	STRAIN-FP-9;		
	RK	MEDLINE=98325194; PubMed=9658122;		
	RA	Laidlaw S.M., Anwar M.A., Thomas W., Green P., Shaw K., Skinner M.A.;		
	RT	"Fowlpox virus encodes nonessential homologs of cellular alpha-SNAP,		
	RL	pC-1, and an orphan human homolog of a secreted nematode protein." ;		
	J. Virol.	72:6742-6751.(1998).		
	CC	-1- CATALYTIC ACTIVITY; HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES		
	CC	SUCCESSFULLY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED		
	CC	OLIGO-NUCLEOTIDES.		
	EMBL:	AJ006408; CAA07014.1; -.		
	DR	InterPro; IPR001604; -.		
	DR	InterPro; IPR002591; -.		
	DR	Pfam; PF01663; Phosphodiesterase; 1.		
	DR	SMART; SM00477; NUC; 1.		
	KW	Hydrolyase.		
	SQ	SEQUENCE	817 AA; 94004 MW; CB68DA0508CC568B CRC64;	
	Query Match	22.9%; Score 1151; DB 14; Length 817;		
	Best Local Similarity	32.4%; Pred. No. 1.9e-85;		
	Matches	263; Conservative 141; Mismatches 276; Indels 132; Gaps		
		21;		
	QY	131	CNTYGVCKGESHWDDCEEIAKAECAGRVREPLLIIFSVDGRASYMKSGSKVMPNIE	190
	Dd	104	CISQVT-----CPPEFERPLLIIANNGRFYLDNWKVEYIPIK	144
	QY	191	KLRSCGTHSPMRPYPTKFPNLYLATGLYPESHGIVGNISMVDVPVDFATFLHREGKF	250

Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF198100; AAF44374.1; -
DR InterPro: IPR001428; -
DR InterPro: IPR001604; -
DR InterPro: IPR002591; -
DR InterPro: IPR003232; -
DR Pfam: PF01663; Phosphodiester; 1.
DR ProDom: PD000946; -; 1.
DR ProDom: PD004900; -; 1.
DR SMART: SM00477; NUC; 1.
SQ SEQUENCE 817 AA; 94038 MW; 8404FD00641DA022 CRC64;

Query Match 22.9%; Score 1151; DB 14; Length 817;
Best Local Similarity 32.4%; Pred. No. 1.9e-85;
Matches 263; Conservative 141; Mismatches 276; Indels 132; Gaps 21;

QY 131 CTNYOVCKGESHWDCCDEEIKAAECAGFVRPLLIIFSVGDFRASYMKKSGKVMNPNI 190
DB 104 CISFQVT-----CPEFERPPIILIAMNGFRDYLNKWEKIPTIK 144
QY 191 KLRSCGTHSPMRVPYPTKTFNLYTLATGLYPESHGIVGNSMYDPVDFATFLRGREF 250
DB 145 DLMEHGVTA-P-MRPVYPTNTPFNLSIVTGLYPISHGITDNEFIDRGTDIEFTIASEETE 203
QY 251 NHRWGGOPLTATKQGVKACTFFW-----SVV-----IPHERILTLRW 292
DB 204 EYEWFGGPIWTTIMKNGFKSATFFPWSGDKVVPKRPTMYRSKSVPEYERINTVLRW 263
QY 293 LTLDPHERSVYAFSEQDFSGHKYGPFGPESSVGSFPTAKRPKRKVAPKRRQRPV 352
DB 264 LKMDTGYRPFYFALYLEEGSGSYEYG----- 290
QY 353 APPKRRRKIIHRMDHYAEATRODKMTNPLREIDKIVQLMDGLKQLKRCVNVIFVGDH 412
DB 291 -----TDDERVCKALEKVDYKALALLMKGLKDLQILGCANLILVSDH 331
QY 413 GMEDVTCRTEPLSNVNLNVDITLVPGLTGRIRSKFSNNAK-YDPKAIANTCTCKKPD 471
DB 332 GMSNVDPKRIKVLKDYITN-NDWIKPGATPVIKQNLNHLRFDYDGIISSTSCVMDQ 390
QY 472 HFKPYLKQHLKRLHYANNRRDTHILLVERHWHVARKPLDVKYKPSGCKFGQDGHGFDN 531
DB 391 PFTVSYRSLPKRLHYSGSFRTEILGVLEEQWSTDENGL-KHRSG-----GFHGSND 444
QY 532 KVNMSQTVFGYGPFTKYKTPPPENIELYNVMDCLLGLKLPAPNGTHGSLNHLRTNT 591
DB 445 SFQDMTAVFLCYGPAFLDDVRPIFDNIELYNMCEILGINPANNNGTVGSLNHLRNSR 504
QY 592 FRP-----TMPEEVRPNYPCIMYLOSDFDLGCTCD--DKVEPKNKLDLNLRLHTKG 642
DB 505 YTHVSSLDIITIESECDRHAYVG-----DHLKGCTCKNIDRFSSKGNKEDSSR---TRS 555
QY 643 STEERHLYGRPAVLY-RTRYDILYHTDFESGYSEIFLMLTSTVTSVQAEVSSVPDHL 701
DB 556 SSYINLPFGKPAVLNRRHHHCIIKNDNYVATYKVNRLPLWTFSI--DITYNSTNIYN 613
QY 702 TSCVRPDRVSPFSQNCILAYKNDKMSYGLFPPVYLSSSPEAKYDAFTVNTVMYPAF 761
DB 614 KTCYLQDRVM-YYPECRKYSTQDVTGYLYP-----ARATFQSLLETNTVPMYRNF 667
QY 762 KRVNMYFORVLVYKASERNGVNYSIGPIFYDYDGLDHTDEKIQO---YVSGSSIPVPT 818
DB 668 KKIWEFVSSILIEVQKHVVNVNMGVPFDSNSNGIRSDWLSMSSGY--NNKYIIFS 725
QY 819 HYSIITSCLTQTPADKCDGPLSVSSILPHRPD-NEESCNSDEDES-KWVEELMKMHT 876
DB 726 DYFVILTYCKDKDSSLNDCYSINIKTESFVPSNDRYYNESCSRENITSVYVRKIFSLHR 785
QY 877 ARVRDIEHLTSLDFFRKTSRSPYEILTKTYL 908
DB 786 VRIKDIEVTSMFSYRNYKTSNNVAYLTKYM 817
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RESULT 15

Q9S082

ID Q9S082 PRELIMINARY; PRT; 457 AA.

AC Q9S082;

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)

DE NUCLEOTIDE PYROPHOSPHATASE-LIKE PROTEIN (EC 3.6.1.9).

GN T16L4.200 OR AT4G29690.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bavan M., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W.,

RA Mayer K.F.X., Lemcke K., Schueller C.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL079344; CAB45329.1; -

DR EMBL: AL161575; CAB79727.1; -

DR InterPro: IPR002591; -

DR Pfam: PF01663; Phosphodiester; 1.

DR Hydrolase.

KW

SQ SEQUENCE 457 AA; 51261 MW; 3B95E6C0AE1B1215 CRC64;

Query Match

Best Local Similarity 32.08%; Score 646.5; DB 10; Length 457;

Matches 151; Conservative 78; Mismatches 136; Indels 107; Gaps 12;

QY 146 DDCEEIKAAECAGFVRPLLIIFSVGDFRASYMKKSGKVMNPNIKLRSCGTHSPY-MRP 204

DB 37 DSSSYVRRPQPKLNKPVVLLISCDFRGYQFKTE--TPNIDLLISRGTEAKTGLIP 94

QY 205 VYPTKTPNLYTLATGLYPESHGIVGNSMYDPVDFATFLRGREFNHRWGGQPLWITA 264

DB 95 VFPTMTFPNHYSTATGLYPASHGIIMNKFTDPVSGELFN---RNLPKMWLGEPLAVTA 150

QY 265 TKQGVKAGTFFW-----SVVTPHERRLITLRLWTLDPHERPSV 303

DB 151 VNQGLMAATYFWPGADYVHKGSWNCPKGCKAPYNSVPLEERVDTILNYFDLPEREIPDF 210

QY 304 YAFVSEQPDFSGHKYGPFGPEESSVGSFPTAKRPKRKVAPKRRQRPVAPPKRRRKIH 363

DB 211 MALYFDEPDIOGHEYGPDDP----- 230

QY 364 RMDHYAAETRQDKMTNPLREIDKIVGQMDGLKOLKLRRCVNVIFVGDHGMEDVTCRTE 423

DB 231 -----RVTEAVSKVDMIGRIIMLEKRVFSDVHVLILGDHGV-TNCDKV 277

QY 424 FLSNLTNVDDITLVPG-----TLGR-TRSKFSNNAKYDPKRAIANLTCCK 468

DB 278 I---YIDDLADWIKIPADWIQDYSPVLAMNPRWGCKVQKNAELVRKMNELSSGKV 334

QY 469 PQQHF-KPYLKQHLKRLHYANNRRIEDIHLVERHWHVARKPLDVKYKPSGCKFFQGDH 527

DB 335 ANGEFLQVYLKENDLPORLHYSDSSRIPPIIGVMGEGMLVKQNTFYQ-----EG--SGTH 387

QY 528 GFONKVNMSQTVFGYGPFTKYKTPPPENIELYNVMDCLLGLKLPAPNGT 579

Db 388 GYDNMFMSRISIFVGYGPRFRGKVPFSFENVQYNAVAEILGLRPAPNGS 439

Search completed: July 19, 2001, 14:46:48
Job time: 171 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:00 ; Search time 34.65 Seconds
(without alignments)
22.745 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213

Perfect score: 76

Sequence: 1 YMRPVPTKTFPN 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*

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22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	13	22 AAY71992	Autotaxin phosphod
2	76	100.0	788	17 AAR86579	Autotaxin derived
3	76	100.0	829	17 AAR86578	Autotaxin derived
4	76	100.0	858	22 AAY71986	Rat autotaxin prot
5	76	100.0	858	22 AAY71995	Rat autotaxin vari
6	76	100.0	858	22 AAY71996	Rat autotaxin vari
7	76	100.0	858	22 AAY71997	Rat autotaxin vari
8	76	100.0	858	22 AAY71998	Rat autotaxin vari
9	76	100.0	858	22 AAY71999	Rat autotaxin vari
10	76	100.0	859	22 AAY71991	Human autotaxin pr
11	76	100.0	863	22 AAY71988	Human teratocarcin

12	76	100.0	915	17 AAR86596	A2058 autotaxin pr
13	76	100.0	915	22 AAY71987	Human melanoma aut
14	76	100.0	979	17 AAR86580	Autotaxin derived
15	71	93.4	849	17 AAR86595	N-tera 2D1 autotax
16	70	92.1	885	22 AAY71989	Rat brain autotaxi
17	69	90.8	873	21 AAY83620	Human PC-1 polypep
18	69	90.8	873	21 AAY83621	Human PC-1 polypep
19	69	90.8	925	16 AAY83621	Variant human PC-1
20	69	90.8	925	20 AAY39355	Human insulin rece
21	69	90.8	925	21 AAB00195	Insulin receptor t
22	49	64.5	400	21 AAG29475	Breast cancer prot
23	49	64.5	457	21 AAG31321	Arabidopsis thalia
24	49	64.5	461	21 AAG29474	Arabidopsis thalia
25	49	64.5	465	21 AAG29473	Arabidopsis thalia
26	43	56.6	173	20 AAY07084	Renal cancer assoc
27	43	56.6	263	18 AAW40374	Human breast cance
28	43	56.6	263	18 AAW01573	Human breast cance
29	43	56.6	263	21 AAY84037	Protein encoded by
30	43	56.6	582	21 AAB53329	Amino acid sequenc
31	43	56.6	579	18 AAW40378	Human colon cancer
32	43	56.6	579	21 AAY84041	Human breast cance
33	42	55.3	411	20 AAY34445	Amino acid sequenc
34	42	55.3	428	20 AAY34324	Porphyromonas ging
35	42	55.3	528	22 AAB79259	Porphyromonas ging
36	42	55.3	530	22 AAB79258	Corynebacterium gl
37	41	53.9	109	19 AAW52839	Secreted protein e
38	41	53.9	453	20 AAY17529	Human secreted pro
39	41	53.9	453	20 AAY02378	Polypeptide identi
40	41	53.9	453	22 AAB90545	Human secreted pro
41	40	52.6	199	21 AAG44375	Arabidopsis thalia
42	40	52.6	199	21 AAG53821	Arabidopsis thalia
43	40	52.6	199	22 AAB68971	Sheep mitosis arre
44	40	52.6	199	22 AAB68972	Human mitosis arre
45	40	52.6	205	18 AAW13020	Human MAD2 protein

ALIGNMENTS

```
RESULT 1
AAY71992
ID AAY71992 standard; peptide; 13 AA.
XX
XX AAY71992;
XX
XX
DT 28-MAR-2001 (first entry)
XX
DE Autotaxin phosphodiesterase catalytic site.
XX
KW Autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity;
KW phosphodiesterase catalytic site.
XX
OS Unidentified.
XX
XX
PN WO200068386-A1.
XX
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US12402.
XX
XX 07-MAY-1999; 99US-0306979.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Kelly JD;
XX
XX WPI; 2001-007397/01.
XX
```

PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 XX obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 PS Disclosure; Page 3; 126pp; English.
 XX
 CC The present sequence is autotaxin phosphodiesterase catalytic
 CC site. Phosphorylation of threonine residue at position 10 of this
 CC sequence is required for autotaxin to undergo autophosphorylation
 CC and exhibit phosphodiesterase and motility-stimulating activities.
 CC Autotaxin is a glycoprotein cytokine which increases
 CC insulin signalling in adipose tissue by producing substrate for
 CC adenosine receptors, resulting in inhibition of lipolysis, and
 CC decreased hepatic gluconeogenesis and serum glucose levels, and
 CC increased insulin sensitivity. It also inhibits differentiation
 CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
 CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
 CC Autotaxin and its analogues are used to stimulate glucose uptake
 CC by cells, particularly to reduce serum glucose levels for
 CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
 CC or generally any condition associated with elevated serum levels
 CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
 CC Transgenic animals that overexpress autotaxin are models for
 CC human metabolic diseases.
 XX
 XX Sequence 13 AA;

Query Match 100.0%; Score 76; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 DB 1 ymrpvpytktfpn 13

RESULT 2
 AAR86579
 ID AAR86579 standard; Protein: 788 AA.
 AC AAR86579;
 XX
 XX 28-JUN-1996 (first entry)
 XX
 DE Autotaxin derived from teratocarcinoma N-tera 2D1 cells.
 XX
 KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
 KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN W09532221-A2.
 PD 30-NOV-1995.
 XX
 PF 24-MAY-1995; 95WO-US06613.
 XX
 PR 28-NOV-1994; 94US-0346455.
 PR 25-MAY-1994; 94US-0249182.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
 XX
 DR WPI: 1996-020533/02.
 DR N-PSDB; AAT06613.
 XX
 PT Autotaxin motility stimulating protein, and DNA encoding it - used
 PT in cancer diagnosis and therapy
 XX
 PS Claim 4; Page 62-65; 112pp; English.
 XX
 CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is

CC an autocrine motility stimulating protein which is present in cancer
 CC cells. ATX stimulates both random and directed migration of melanoma
 CC cells. The tumorous form of ATX is a secreted protein, while the
 CC transmembrane bound form is not present in tumour cells. The cDNA
 CC encoding this sequence can be used in a vector, to transform cells. The
 CC recombinant cells can then be used to produce the peptide sequences.
 CC Antibodies specific for these sequences can be produced, and can be used
 CC in cancer diagnosis and therapy. Different sites of localisation of the
 CC protein are utilised for diagnosis and prognosis of the stages of tumour
 CC progression. The sequences can be used in treatment methods to
 CC advantageously block the activity of the secreted form of ATX, while
 CC having little effect on the membrane form of ATX.
 XX

SQ Sequence 788 AA;

Query Match 100.0%; Score 76; DB 17; Length 788;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 DB 126 ymrpvpytktfpn 138

RESULT 3
 AAR86578
 ID AAR86578 standard; Protein: 829 AA.
 AC AAR86578;
 XX

DT 28-JUN-1996 (first entry)
 XX
 DE Autotaxin derived from melanoma cell line A2058.
 XX

KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
 KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
 XX

OS Homo sapiens.
 XX

PN W09532221-A2.
 XX

PD 30-NOV-1995.
 XX

PF 24-MAY-1995; 95WO-US06613.
 XX

PR 28-NOV-1994; 94US-0346455.
 PR 25-MAY-1994; 94US-0249182.
 XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX

PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
 XX

DR WPI: 1996-020533/02.
 DR N-PSDB; T06612.
 XX

PT Autotaxin motility stimulating protein, and DNA encoding it - used
 PT in cancer diagnosis and therapy
 XX
 PS Claim 4; Page 57-60; 112pp; English.

CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is
 CC an autocrine motility stimulating protein which is present in cancer
 CC cells. ATX stimulates both random and directed migration of melanoma
 CC cells. The tumorous form of ATX is a secreted protein, while the
 CC transmembrane bound form is not present in tumour cells. The cDNA
 CC encoding this sequence can be used in a vector, to transform cells. The
 CC recombinant cells can then be used to produce the peptide sequences.
 CC Antibodies specific for these sequences can be produced, and can be used
 CC in cancer diagnosis and therapy. Different sites of localisation of the
 CC protein are utilised for diagnosis and prognosis of the stages of tumour
 CC progression. The sequences can be used in treatment methods to
 CC advantageously block the activity of the secreted form of ATX, while

CC having little effect on the membrane form of AXT.

XX Sequence 829 AA;

Query Match 100.0%; Score 76; DB 17; Length 829;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13

Db 115 ymrpvyptktpn 127

RESULT 4

ID AAY71986 standard; Protein; 858 AA.

XX AC AAY71986;

DT 28-MAR-2001 (first entry)

DE Rat autotaxin protein.

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity.

OS Rattus sp.

XX Key Location/Qualifiers

FT Domain 5..15

FT Binding-site 122..124 /note= "Putative transmembrane domain"

FT Region 143..158 /label= RGD_binding_domain

FT Region 149..158 /label= Epitope

FT Region 149..158 /label= Epitope

FT /note= "This region is specifically claimed in claim 10;
 This region is absent in rat brain autotaxin designated
 as PD-Talpha sequence (AAY71989)."

FT Active-site 196..208

FT Region 585..595 /note= "Autotaxin phosphodiesterase catalytic site"

FT /label= Epitope

FT /note= "This region is specifically claimed in claim 10"

XX WO200068386-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12402.

XX 07-MAY-1999; 99US-0306979.

XX (ZYMO) ZYMOGENETICS INC.

XX Kelly JD;

XX WPI; 2001-007397/01.

DR N-PSDB; AAD02131.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX Claim 1; Page 101-104; 126pp; English.

XX The present sequence is rat autotaxin protein. Autotaxin is a

CC glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic
 CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.

XX Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13

Db 196 ymrpvyptktpn 208

RESULT 5

AAV71995

ID AAY71995 standard; Protein; 858 AA.

XX AC AAY71995;

XX 28-MAR-2001 (first entry)

DE Rat autotaxin variant (A93V).

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; variant.

OS Rattus sp.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 93

FT /note= "Wild type Ala substituted by Val"

XX WO200068386-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12402.

XX 07-MAY-1999; 99US-0306979.

XX (ZYMO) ZYMOGENETICS INC.

XX Kelly JD;

XX WPI; 2001-007397/01.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX Disclosure; Page -; 126pp; English.

XX The present sequence is variant (A93V) of rat autotaxin protein.

CC Autotaxin is a glycoprotein cytokine which increases insulin

CC signalling in adipose tissue by producing substrate for adenosine

CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (AAY71986).
 CC
 XX
 SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 196 ymrpvptktfnp 208

RESULT 6
 AAY71996
 ID AAY71996 standard; Protein; 858 AA.
 XX
 AC AAY71996;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Rat autotaxin variant (A194V).
 XX
 KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; variant.
 XX
 OS Rattus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 194 /note= "Wild type Ala substituted by Val"
 FT
 XX
 PN WO200068386-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000WO-US12402.
 XX
 PR 07-MAY-1999; 99US-0306979.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Kelly JD;
 XX
 DR WPI; 2001-007397/01.
 DR
 PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX
 PS Disclosure; Page -: 126pp; English.
 XX
 CC The present sequence is variant (A194V) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (AAY71986).
 CC
 XX
 SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 196 ymrpvptktfnp 208

RESULT 7
 AAY71997
 ID AAY71997 standard; Protein; 858 AA.
 XX
 AC AAY71997;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Rat autotaxin variant (S236T).
 XX
 KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; variant.
 XX
 OS Rattus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 236 /note= "Wild type Ser substituted by Thr"
 FT
 XX
 PN WO200068386-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000WO-US12402.
 XX
 PR 07-MAY-1999; 99US-0306979.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Kelly JD;
 XX
 DR WPI; 2001-007397/01.
 DR
 PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX
 PS Disclosure; Page -: 126pp; English.
 XX
 CC The present sequence is variant (S236T) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (AAV71986).
 CC
 XX SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
 |||||
 Db 196 ymrpvpyptktpn 208

RESULT 8
 AAV71998
 ID AAV71998 standard; Protein; 858 AA.
 XX
 AC AAV71998;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Rat autotaxin variant (R265K).
 XX
 KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
 XX
 OS Rattus sp.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 265 /note= "Wild type Arg substituted by Lys"
 FT

XX WO200068386-A1.
 XX
 XX 16-NOV-2000.
 XX
 XX 05-MAY-2000; 2000WO-US12402.
 XX
 XX 07-MAY-1999; 99US-0306979.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Kelly JD;
 XX
 XX WPI; 2001-007397/01.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 PT
 XX Disclosure; Page -: 126pp; English.

XX The present sequence is variant (R265K) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (AAV71986).
 CC
 XX SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
 |||||
 Db 196 ymrpvpyptktpn 208

RESULT 9
 AAV71999
 ID AAV71999 standard; Protein; 858 AA.
 XX
 AC AAV71999;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Rat autotaxin variant (S289T).
 XX
 KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
 XX
 OS Rattus sp.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 289 /note= "Wild type Ser substituted by Thr"
 FT

XX WO200068386-A1.
 XX
 XX 16-NOV-2000.
 XX
 XX 05-MAY-2000; 2000WO-US12402.
 XX
 XX 07-MAY-1999; 99US-0306979.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Kelly JD;
 XX
 XX WPI; 2001-007397/01.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 PT
 XX Disclosure; Page -: 126pp; English.

XX The present sequence is variant (S289T) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (RAY71986).
 CC
 SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 196 ymrpvpytktfpn 208

RESULT 10
 AAY71991
 ID AAY71991 standard; Protein; 859 AA.
 AC AAY71991;
 XX
 XX 28-MAR-2001 (first entry)
 DT Human autotaxin protein.
 DE
 DE Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Domain 8..26
 FT /note= "Putative transmembrane domain"
 FT Cleavage-site 44..45
 FT Binding-site 123..125
 FT /label= RGD_binding_domain
 FT Active-site 197..209
 FT /note= "Putative phosphodiesterase active site"
 XX
 XX WO200068386-A1.
 PN
 XX
 XX 16-NOV-2000.
 PD
 XX
 XX 05-MAY-2000; 2000WO-US12402.
 PF
 XX
 XX 07-MAY-1999; 99US-0306979.
 PR
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX
 XX Kelly JD;
 PI
 XX
 XX WPI; 2001-007397/01.
 DR N-PSDB; AAD02133.
 DR
 XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 PT
 XX Claim 27; Page 119-121; 126pp; English.
 PS

XX The present sequence is human autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases
 CC insulin signalling in adipose tissue by producing substrate for
 CC adenosine receptors, resulting in inhibition of lipolysis,
 CC decreased hepatic gluconeogenesis and serum glucose levels, and
 CC increased insulin sensitivity. It also inhibits differentiation
 CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
 CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
 CC Autotaxin and its analogues are used to stimulate glucose uptake
 CC by cells, particularly to reduce serum glucose levels for
 CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
 CC or generally any condition associated with elevated serum levels
 CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
 CC Transgenic animals that overexpress autotaxin are models for
 CC human metabolic diseases.
 XX
 SQ Sequence 859 AA;

Query Match 100.0%; Score 76; DB 22; Length 859;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 197 ymrpvpytktfpn 209

RESULT 11
 AAY71988
 ID AAY71988 standard; Protein; 863 AA.
 XX
 AC AAY71988;
 XX
 XX 28-MAR-2001 (first entry)
 DT Human teratocarcinoma autotaxin.
 DE
 DE Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; teratocarcinoma.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Binding-site 127..129
 FT /label= RGD_binding_domain
 FT Active-site 201..213
 FT /note= "Autotaxin phosphodiesterase catalytic site"
 XX
 XX WO200068386-A1.
 PN
 XX
 XX 16-NOV-2000.
 PD
 XX
 XX 05-MAY-2000; 2000WO-US12402.
 PF
 XX
 XX 07-MAY-1999; 99US-0306979.
 PR
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX
 XX Kelly JD;
 PI
 XX
 XX WPI; 2001-007397/01.
 DR
 XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 PT
 XX Claim 27; Page 108-110; 126pp; English.
 PS
 XX

CC The present sequence is autotaxin isolated from human
 CC teratocarcinoma cells. Autotaxin is a glycoprotein cytokine which
 CC increases insulin signalling in adipose tissue by producing substrate
 CC for adenosine receptors, resulting in inhibition of lipolysis,
 CC decreased hepatic gluconeogenesis and serum glucose levels, and
 CC increased insulin sensitivity. It also inhibits differentiation
 CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
 CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
 CC Autotaxin and its analogues are used to stimulate glucose uptake
 CC by cells, particularly to reduce serum glucose levels for
 CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
 CC or generally any condition associated with elevated serum levels
 CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
 CC Transgenic animals that overexpress autotaxin are models for
 CC human metabolic diseases.

XX Sequence 863 AA;

Query Match 100.0%; Score 76; DB 22; Length 863;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YMRPVYPTKTFPN 13
 |||||
 Db 201 ymrpvptktfnp 213

RESULT 12

AAR86596
 ID AAR86596 standard; Protein; 915 AA.

XX AAR86596;

XX 01-JUL-1996 (first entry)

XX A2058 autotaxin protein.

XX Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
 KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.

XX Homo sapiens.

XX W09532221-A2.

XX 30-NOV-1995.

XX 24-MAY-1995; 95WO-US06613.

XX 28-NOV-1994; 94US-0346455.

XX 25-MAY-1994; 94US-0249182.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Krutzh J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX WPI; 1996-020533/02.

XX Autotaxin motility stimulating protein, and DNA encoding it - used
 PT in cancer diagnosis and therapy

XX Claim 4; Page 91-94; 112pp; English.

XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This
 CC sequence represents the full length protein sequence of the A2058
 CC melanoma cell line ATX protein. ATX is an autocrine motility
 CC stimulating protein which is present in cancer cells. ATX stimulates
 CC both random and directed migration of melanoma cells. The tumourous form
 CC of ATX is a secreted protein, while the transmembrane bound form is not
 CC present in tumour cells. The cDNA encoding this sequence can be used in
 CC a vector, to transduce cells. The recombinant cells can then be used to
 CC produce the peptide sequences. Antibodies specific for these sequences
 CC can be produced, and can be used in cancer diagnosis and therapy.

CC Different sites of localisation of the protein are utilised for diagnosis
 CC and prognosis of the stages of tumour progression. The sequences can be
 CC used in treatment methods to advantageously block the activity of the
 CC secreted form of ATX, while having little effect on the membrane form of
 CC ATX.

XX Sequence 915 AA;

Query Match 100.0%; Score 76; DB 17; Length 915;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YMRPVYPTKTFPN 13
 |||||
 Db 201 ymrpvptktfnp 213

RESULT 13

AAY71987
 ID AAY71987 standard; Protein; 915 AA.

XX AAY71987;

XX 28-MAR-2001 (first entry)

XX Human melanoma autotaxin.

XX Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; melanoma.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Binding-site 127..129
 FT /label= RGD_binding_domain
 FT Active-site 201..213

FT /note= "Autotaxin phosphodiesterase catalytic site"
 XX W0200068386-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12402.

XX 07-MAY-1999; 99US-0306979.

XX (ZYMO) ZYMOGENETICS INC.

XX Kelly JD;

XX WPI; 2001-007397/01.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 PT Claim 27; Page 105-108; 136pp; English.

XX The present sequence is autotaxin isolated from human melanoma
 CC cells. Autotaxin is a glycoprotein cytokine which increases
 CC insulin signalling in adipose tissue by producing substrate for
 CC adenosine receptors, resulting in inhibition of lipolysis,
 CC decreased hepatic gluconeogenesis and serum glucose levels, and
 CC increased insulin sensitivity. It also inhibits differentiation
 CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
 CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
 CC Autotaxin and its analogues are used to stimulate glucose uptake
 CC by cells, particularly to reduce serum glucose levels for
 CC treatment of non-insulin dependent diabetes (NIDDM) in humans,

CC sequences can be produced, and can be used in cancer diagnosis and
CC therapy. Different sites of localisation of the protein are utilised for
CC diagnosis and prognosis of the stages of tumour progression. The
CC sequences can be used in treatment methods to advantageously block the
CC activity of the secreted form of AXT, while having little effect on the
CC membrane form of AXT.

XX
SQ Sequence 849 AA;

Query Match 93.4%; Score 71; DB 17; Length 849;
Best Local Similarity 92.3%; Pred. No. 0.00091;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
Db 201 hmrpvyptktfnp 213

Search completed: July 19, 2001, 14:45:00
Job time: 208 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:54 ; Search time 25.97 Seconds
(without alignments)
38.131 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213

Perfect score: 76

Sequence: 1 YMRPVPTKTFPN 13

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	915	1 A55144	autotaxin precursor
2	70	92.1	885	1 A55453	plasma cell membra
3	69	90.8	96	2 A25274	phosphodiesterase
4	69	90.8	300	2 A11179	protein kinase PC-
5	69	90.8	925	1 A39216	plasma cell membra
6	66	86.8	905	1 A27410	plasma cell membra
7	65	85.5	875	1 A57080	cell surface antiq
8	54	71.1	493	2 S50443	hypothetical prote
9	50	65.8	743	2 S19437	hypothetical prote
10	49	64.5	457	2 T09932	nucleotide pyropho
11	49	64.5	461	2 T09933	nucleotide pyropho
12	49	64.5	829	2 T19494	hypothetical prote
13	48	63.2	496	2 T09931	nucleotide pyropho
14	47	61.8	479	2 T03293	nucleotide pyropho
15	45	59.2	674	2 T19495	hypothetical prote
16	44.5	58.6	316	2 S46237	glucan endo-1,3-be
17	42	55.3	429	2 T33724	hypothetical prote
18	41	53.9	247	2 T32514	hypothetical prote
19	41	53.9	381	2 T23250	hypothetical prote
20	41	53.9	427	2 S57776	cysteine proteinas
21	41	53.9	433	2 B82537	phosphodiesterase
22	41	53.9	493	2 T01206	cysteine proteinas
23	41	53.9	1829	2 T24583	hypothetical prote
24	40	52.6	174	2 S15391	crustacyanin chain
25	40	52.6	205	2 G01942	mitotic feedback c
26	40	52.6	247	2 T45847	hypothetical prote
27	40	52.6	346	2 J80159	cysteine proteinas
28	40	52.6	466	2 T06416	cysteine proteinas
29	40	52.6	1547	2 JQ0096	hypothetical 176K

30	39	51.3	269	2 A84841	probable embryo-ab
31	39	51.3	321	2 E86423	hypothetical prote
32	39	51.3	453	2 T16795	hypothetical prote
33	39	51.3	471	2 G69809	aminocid carrier
34	39	51.3	485	2 T40657	probable phosphodie
35	39	51.3	528	2 F64580	hypothetical prote
36	39	51.3	528	2 F71931	outer membrane pro
37	39	51.3	1084	2 S52887	serine/threonine-s
38	38	50.0	256	2 T49254	Myb DNA binding pr
39	38	50.0	453	2 S67089	hypothetical prote
40	38	50.0	567	2 C27698	hypothetical prote
41	38	50.0	604	2 S24760	hydroxymethylgluta
42	38	50.0	708	2 T48022	hypothetical prote
43	38	50.0	791	2 T39924	hypothetical prote
44	38	50.0	1068	2 E81965	probable outer mem
45	38	50.0	1082	2 H81020	serotype-1-specifi

ALIGNMENTS

RESULT 1

A55144
autotaxin precursor - human
N:Contains: phosphodiesterase I (EC 3.1.4.1)
C:Species: Homo sapiens (man)
C:date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Murata, J.; Lee, H.Y.; Clair, T.; Kruttsch, H.C.; Arestad, A.A.; Sobel, M.E.; Liott
C:Accession: A55144; A42329
J. Biol. Chem. 269, 30479-30484, 1994
A:title: cDNA cloning of the human tumor motility-stimulating protein, autotaxin, rev
A:Reference number: A55144; MUID:95074054
A:Accession: A55144
A:Molecule type: mRNA
A:Residues: 1-915 <MUR>
A:Cross-references: GB:L35594; NID:9537905; PIDN:AAA64785.1; PID:9537906
A:Note: Parts of this sequence were confirmed by peptide sequencing
R:Stracke, M.L.; Kruttsch, H.C.; Unsworth, E.J.; Arestad, A.; Cioce, V.; Schiffmann,
J. Biol. Chem. 267, 2524-2529, 1992
A:title: Identification, purification, and partial sequence analysis of autotaxin, a
A:Reference number: A42329; MUID:92129337
A:Accession: A42329
A:Molecule type: protein
A:Residues: 256-266;422-444;504-507,'AN';510,'X',511-515;533-548;'S',554-559,'N',561-
A:Experimental source: A2058 melanoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:78526, NCBIP:78523, NCBIP:78521,
A:Note: a peptide fragment Tyr-Asp-Val-Pro-Trp-Asn-Glu-Thr-Ile was also found
C:Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.
C:Genetics:
A:Gene: GDB:ATX
A:Cross-references: GDB:378346
A:Map position: 8q22-8qter
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase
F:55-98/Domain: somatomedin B homology <SBH1>
F:99-142/Domain: somatomedin B homology <SBH2>
F:54,463,577,859/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:210/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 100.0%; Score 76; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVPTKTFPN 13

Db 201 YMRPVPTKTFPN 213

RESULT 2

A55453
plasma cell membrane glycoprotein PC-1, brain specific - rat
N:Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)

Qy	1	YMRPVYPTKTFPN	13
		I : I I I I I I I I	
Db	30	YLRPAYPTKTFPN	42

A:Reference number: S51030; MUID:95094801
A:Accession: S51030
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-80 <BEL>
C:Genetics:
A:Gene: GDB:PDNP1; M6S1; NPFS
A:Cross-references: GDB:132615; OMIM:173335
A:Map position: 6q22-q23
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; transmembrane
F:77-97/Domain: transmembrane #status predicted <TMM>
F:104-144/Domain: somatomedin B homology <SBH1>
F:145-198/Domain: somatomedin B homology <SBH2>
F:179,285,341,477,578,585,643,700,731,748/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:256/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 90.8%; Score 69; DB 1; Length 925;
Best Local Similarity 100.0%; Pred. No. 0.0009; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVPTKTFPN 13
||| |||||
Db 248 MRPVPTKTFPN 259
||| |||||

RESULT 6
A27410
plasma cell membrane glycoprotein PC-1 - mouse
N:Alternate names: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.1.1)
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C:Accession: A27410; I59055; S38354
R:van Driel, I.R.; Goding, J.W.
J. Biol. Chem. 262, 4882-4887, 1987
A:Title: Plasma cell membrane glycoprotein PC-1. Primary structure deduced from cDNA cloning
A:Reference number: A27410; MUID:87165306
A:Accession: A27410
A:Molecule type: mRNA
A:Residues: 1-905 <VAN>
A:Cross-references: GB:J02700; NID:q200236; PIDN:AAA39893.1; PID:q200237
A>Note: the authors translated the codon CAG for residue 24 as Glu
R:van Driel, I.R.; Wilks, A.F.; Pietersz, G.A.; Goding, J.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8619-8623, 1985
A:Title: Murine plasma cell membrane antigen PC-1: Molecular cloning of cDNA and analysis
A:Reference number: I59055; MUID:86094275
A:Accession: I59055
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 203-219 <RES>
A:Cross-references: GB:M12552; NID:q200234; PIDN:AAA39892.1; PID:q200235
R:Belli, S.I.; van Driel, I.R.; Goding, J.W.
Eur. J. Biochem. 217, 421-428, 1993
A:Title: Identification and characterization of a soluble form of the plasma cell membrane antigen PC-1
A:Reference number: S38354; MUID:94039066
A:Accession: S38354
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 35-219 <BEL>
A:Cross-references: EMBL:104516
C:Genetics:
A:Introns: 62/3; 87/1; 126/1; 168/1; 188/2
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; transmembrane
F:86-126/Domain: somatomedin B homology <SBH1>
F:127-170/Domain: somatomedin B homology <SBH2>
F:161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:238/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 86.8%; Score 66; DB 1; Length 905;
Best Local Similarity 91.7%; Pred. No. 0.0028;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVPTKTFPN 13
||| |||||
Db 230 MRPVPTKTFPN 241
||| |||||

RESULT 7
A57080
cell surface antigen RB13-6 - rat
N:Contains: phosphodiesterase I (EC 3.1.4.1)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A57080
R:Deisler, H.; Lotspeich, F.; Rajewsky, M.F.
J. Biol. Chem. 270, 9849-9855, 1995
A:Title: Affinity purification and cDNA cloning of rat neural differentiation and tumorigenesis
A:Reference number: A57080; MUID:95247775
A:Accession: A57080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-875 <DEI>
A:Cross-references: GB:247987; NID:q806378; PIDN:CAA88029.1; PID:q806379
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase; transmembrane
F:1-22/Domain: cytosolic #status predicted <CYT>
F:23-45/Domain: transmembrane #status predicted <TMM>
F:46-875/Domain: extracellular #status predicted <EXT>
F:51-94/Domain: somatomedin B homology <SBH>
F:95-138/Domain: somatomedin B homology <SBH2>
F:206/Binding site: AMP (Thr) (covalent) #status predicted
F:237,280,289,533,574,594,702,789/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.5%; Score 65; DB 1; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0041; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVPTKTFPN 13
||| |||||
Db 197 YMRPVPTKTFPN 209
||| |||||

RESULT 8
S50443
hypothetical protein YEL016c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 29-Oct-1999
C:Accession: S50443
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: Saccharomyces cerevisiae chromosome V cosmid 9871, 8199, 9867, 9495 a
A:Reference number: S50428
A:Accession: S50443
A:Molecule type: DNA
A:Residues: 1-493 <DIE>
A:Cross-references: EMBL:U18530; NID:g602367; PID:g602383; GSPDB:GN00005; MIPS:YEL016
C:Genetics:
A:Gene: MIPS:YEL016c
A:Map position: 5L

Query Match 71.1%; Score 54; DB 2; Length 493;
Best Local Similarity 69.2%; Pred. No. 0.17; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVPTKTFPN 13
||| |||||
Db 118 YMRPVPTKTFPN 130
||| |||||

RESULT 9
S19437

```

Query Match      64.5%; Score 49; DB 2; Length 461;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 PVYPTKTTPN 13
      ||| || |||
Db      97 PVFPTMTTPN 106

RESULT 12
T19494
hypothetical protein C27A7.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19494

```

Submitted to the EMBL data library, October 1996

A;Reference number: Z19132
A;Accession: T19494
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-829 <MIL>
A;Cross-references: EMBL:Z81041; PIDN:CAR82784.1; GSPDB:GN00023; CESP:C27A7.1
A;Experimental source: clone C27A7
C;Genetics:
A;Gene: CESP:C27A7.1
A;Map position: 5
A;Introns: 12/3; 37/1; 100/3; 176/2; 272/3; 392/1; 427/1; 479/2; 566/2; 588/3; 677/1;

A:Gene: CESP/C2/A.1
 A:Map position: 5
 A:Introns: 12/3; 37/1; 100/3; 176/2; 272/3; 392/1; 427/1; 479/2; 566/2; 588/3; 677/1;
 Query Match 64.5% Score 49; DB 2; Length 829;
 Best Local Similarity 80.0% Pred. No. 2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

C;Accession: T09931
R;Revan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, June 1999
A;Reference number: 216897
A;Accession: T09931
A;Molecule type: DNA
A;Residues: 1-496 <BEV>
A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190
A;Experimental source: cultivar Columbia; BAC clone T16L4
C;Genetics:
A;Gene: ATSP:T16L4.190
A;Map position: 4

Query Match 63.2%; Score 48; DB 2; Length 496;
 Best Local Similarity 80.0%; Pred. No. 1.8;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PVYPTKTFPN 13

||:|||||

Db 146 PVFPTLTFPN 155

RESULT 14

T03293
 nucleotide pyrophosphatase homolog - rice
 C:Species: Oryza sativa (rice)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
 C:Accession: T03293
 R:Hsing, Y.C.; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.
 submitted to the EMBL Data Library, April 1995
 A:Description: Rice early embryogenesis gene.
 A:Reference number: 214889
 A:Accession: T03293
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-479 <HSI>
 A:Cross-references: EMBL:U25430; NID:g818848; PID:g818849
 A:Experimental source: strain Tainung 67
 C:Genetics:
 A:Note: OSE4

Query Match 61.8%; Score 47; DB 2; Length 479;
 Best Local Similarity 70.0%; Pred. No. 2.5;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PVYPTKTFPN 13

||:|||||

Db 129 PIFPTLTFPN 138

RESULT 15

T19495
 hypothetical protein C27A7.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19495
 R:Harris, B.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19132
 A:Accession: T19495
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-674 <WIL>
 A:Cross-references: EMBL:Z81041; PIDN:CAB02785.1; GSPDB:GN00023; CESP:C27A7.3
 A:Experimental source: clone C27A7
 C:Genetics:
 A:Gene: CESP:C27A7.3
 A:Map position: 5
 A:Introns: 61/1; 98/3; 191/1; 220/3; 268/3; 340/1; 392/2; 475/2; 496/3; 537/1; 588/1

Query Match 59.2%; Score 45; DB 2; Length 674;
 Best Local Similarity 70.0%; Pred. No. 7.7;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PVYPTKTFPN 13

||:|||||

Db 166 PSFSTKTFPN 175

Search completed: July 19, 2001, 14:45:55
 Job time: 153 sec

Result No.	Query Match	Score	Length	DB	ID	Description	§
1	69	90.8	61	1	PPDL_BOVIN	P15396 bos taurus	
2	69	90.8	873	1	PCL_HUMAN	P22413 homo sapien	
3	66	86.8	871	1	PCL_MOUSE	P06802 mus musculus	
4	54	71.1	493	1	YEB6_YEAST	P39997 saccharomyc	
5	50	65.8	716	1	YCR6_YEAST	P25353 saccharomyc	
6	44.5	58.6	343	1	E13E_HORVU	Q02438 hordeum vul	
7	42	55.3	743	1	BGAL_THEST	P77989 thermoanaer	
8	40	52.6	174	1	CRN2_HOMGA	P80007 homarus gam	
9	40	52.6	205	1	MD21_HUMAN	Q13257 homo sapien	
10	40	52.6	205	1	MD21_MOUSE	Q921b5 mus musculus	
11	40	52.6	346	1	CYSL_LYCRS	P20721 lycopersico	
12	40	52.6	1547	1	RPO_PMV	P20951 papaya mosa	
13	39	51.3	595	1	HMD2_SOLITU	Q1437 solanum tub	
14	39	51.3	890	1	YCF2_MESVI	Q9mp8 mesostigma	
15	39	51.3	1064	1	KINI_YEARST	P13185 saccharomyc	
16	38	50.0	172	1	CH18_DROME	P07184 drosophila	
17	38	50.0	604	1	HMDH_NICSV	Q01559 nicotiana s	
18	37	48.7	177	1	CRAB_SQUAC	Q02512 squalus acu	
19	37	48.7	232	1	H823_MOUSE	P04231 mus musculu	
20	37	48.7	264	1	H821_MOUSE	P04230 mus musculu	
21	37	48.7	264	1	H822_MOUSE	P01915 mus musculu	
22	37	48.7	264	1	H824_MOUSE	P20040 mus musculu	
23	37	48.7	264	1	H821_MOUSE	P18468 mus musculu	
24	37	48.7	264	1	H82J_MOUSE	P18469 mus musculu	
25	37	48.7	328	1	GPT_SULAC	P39465 sulfolobus	
26	37	48.7	333	1	PAP2_VACCC	P21033 vaccinia vi	
27	37	48.7	333	1	PAP2_VACCV	P07617 vaccinia vi	
28	37	48.7	333	1	PAP2_VARV	P33052 variola vir	
29	37	48.7	480	1	SYFA_METTA	Q57911 methanococc	
30	37	48.7	602	1	HMD2_LYCRS	P48022 lycopersico	
31	37	48.7	636	1	UBA2_YEAST	P52488 saccharomyc	
32	37	48.7	3358	1	PGCV_MOUSE	Q62059 mus musculu	
33	37	48.7	3866	1	HRX_MOUSE	P55200 mus musculu	

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91009202; PubMed=2211644;
 RA Buckley M.F., Loveland K.A., McKinstry W.J., Carson O.M., Goding J.W.;
 RT "Buckley M.F., Loveland K.A., McKinstry W.J., Carson O.M., Goding J.W.;
 RT "Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human
 RT molecule, amino acid sequence, and chromosomal location.";
 RL J. Biol. Chem. 265:17506-17511(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92246539; PubMed=1315502;
 RA Funakoshi I., Kato H., Horie K., Yano T., Hori Y., Kobayashi H.,
 RA Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T.,
 RA Yamashina I.;
 RT "Molecular cloning of cDNAs for human fibroblast nucleotide
 RT pyrophosphatase.";
 RL Arch. Biochem. Biophys. 295:180-187(1992).
 RN [3]
 RP SEQUENCE OF 93-133 FROM N.A., AND VARIANT GLN-121.
 RX MEDLINE=99408501; PubMed=10480624;
 RA Pizzuti A., Frittitta L., Argiolas A., Baratta R., Goldfine I.D.,
 RA Bozzali M., Ercolino T., Scarlato G., Iacoviello L., Vigneri R.,
 RA Tassi V., Trischitta V.;
 RT "A polymorphism (K121Q) of the human glycoprotein PC-1 gene coding
 RT region is strongly associated with insulin resistance.";
 RL Diabetes 48:1891-1894(1999).
 CC -1- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
 CC -1- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSFULLY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 CC OLIGO-NUCLEOTIDES.
 CC -1- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER
 CC OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE
 CC OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.
 CC -1- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.
 CC
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 CC
 DR EMBL: M57736; AAA63237.1; -;
 DR EMBL: D12485; BAA02054.1; -;
 DR EMBL: D12485; BAA02053.1; ALT_INIT.
 DR EMBL: AF067177; AAD38420.1; -;
 DR EMBL: AF067178; AAD38421.1; -;
 DR PIR: A39216; A39216.
 DR MIM: 173335; -;
 DR InterPro: IPR001212; -;
 DR InterPro: IPR002591; -;
 DR Pfam: PF01663; Phosphodiester; 1.
 DR Pfam: PF01033; Somatomedin B; 2.
 DR PRINTS: PR00022; SOMATOMEDIN.
 DR PROSITE: PS00524; SOMATOMEDIN_B; 2.
 KW Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase;
 RN Polymorphism.
 FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 25 45 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN).
 FT DOMAIN 46 873 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 52 92 SOMATOMEDIN-B LIKE.
 FT DOMAIN 93 136 SOMATOMEDIN-B LIKE.
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 425 425 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 696 696 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 121 121 K -> Q.
 FT /FTIG=VAR_008873.
 SQ SEQUENCE 873 AA: 99929 MW: 872808C20B048070 CRC64;
 Query Match 90.8%; Score 69; DB 1; Length 873;
 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MRPVYPTKTFPN 13
 Db 196 MRPVYPTKTFPN 207
 |||||
 RESULT 3
 PCL_MOUSE
 ID PCL_MOUSE STANDARD; PRT; 871 AA.
 AC P06802;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE
 DE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE
 DE (EC 3.6.1.9) (NPPASE)].
 GN PDNFI OR PC1 OR NPPS.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX MEDLINE=87165906; PubMed=3104326;
 RA van Driel I.R., Goding J.W.;
 RT "Plasma cell membrane glycoprotein PC-1. Primary structure deduced
 RT from cDNA clones.";
 RL J. Biol. Chem. 262:4882-4887(1987).
 RN [1]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=85056299; PubMed=3917281;
 RA Stearne P.A., van Driel I.R., Grego B., Simpson R.J., Goding J.W.;
 RT "The murine plasma cell antigen PC-1: purification and partial amino
 RT acid sequence.";
 RL J. Immunol. 134:443-448(1985).
 RN [3]
 RP FUNCTION, AND SEQUENCE FROM N.A.
 RX MEDLINE=91271356; PubMed=1647027;
 RA Rebbe N.F., Tong B.D., Finley E.M., Hickman S.;
 RT "Identification of nucleotide pyrophosphatase/alkaline
 RT phosphodiesterase I activity associated with the mouse plasma cell
 RT differentiation antigen PC-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5192-5196(1991).
 RN [4]
 RP SEQUENCE OF 169-185 FROM N.A.
 RX MEDLINE=86094275; PubMed=3001713;
 RA van Driel I.R., Wilks A.F., Pietersz G.A., Goding J.W.;
 RT "Murine plasma cell membrane antigen PC-1: molecular cloning of cDNA
 RT and analysis of expression.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:8619-8623(1985).
 CC -1- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
 CC -1- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSFULLY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 CC OLIGO-NUCLEOTIDES.
 CC -1- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED ON THE SURFACE OF
 CC ANTIBODY-SECRETING CELLS.
 CC -1- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.
 CC
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CC -----
DR EMBL; U18530; AAB64493.1; -
DR SGD; S0000742; YEL016C.
DR InterPro; IPR002591; -
DR Pfam; PF01663; Phosphodiester; 1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 57354 MW; 10E67A05C6DEDF09 CRC64;

Query Match 71.1%; Score 54; DB 1; Length 493;
Best Local Similarity 69.2%; Pred. No. 0.063;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
DB 118 YMIPSPTPTTFPN 130
||| :||:||||

RESULT 5
YCR6_YEAST STANDARD; PRT; 743 AA.
ID YCR6_YEAST
AC P25353;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOHETICAL 84.9 KDA PROTEIN IN PMP1-FEN2 INTERGENIC REGION.
GN YCR026C OR YCR26C OR YCR246.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-244 FROM N.A.
RA Pohl F., Richterich P., Wurst H.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 244-743 FROM N.A.
RX MEDLINE-92245758; PubMed-1574926;
RA Bolle P.-A., Gilliquet V., Berben G., Dumont J., Hilger F.;
RT "The complete sequence of K3B, a 7.9 kb fragment between POK1 and
RT CRY1 on chromosome III, reveals the presence of seven open reading
RT frames.";
RL Yeast 8:205-213(1992).
CC -1- SIMILARITY: TO YEAST YEL016C.
CC -----
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CC -----
DR EMBL; X59720; CAA42318.1; -
DR PIR; S19437; S19437.
DR PIR; S27380; S27380.
DR SGD; S0000621; YCR026C.
DR InterPro; IPR002591; -
DR Pfam; PF01663; Phosphodiester; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 114 135 POTENTIAL.
SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

Query Match 65.8%; Score 50; DB 1; Length 743;
Best Local Similarity 61.5%; Pred. No. 0.47;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
DB 210 FMIPSPTPTTFPN 222
||| :||:||||

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CC -----
DR EMBL; J02700; AAA39893.1; ALT_INIT.
DR EMBL; M12552; AAA39892.1; -
DR PIR; A27410; A27410.
DR MGD; MGI:97370; Pdnpl.
DR InterPro; IPR001212; -
DR Pfam; PF01663; Phosphodiester; 1.
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PRO0022; SOMATOMEDIN_B; 2.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
KW Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase.
FT MOD_RES ?1 ?1
FT DOMAIN 1 24
FT TRANSMEM 25 45
FT DOMAIN 46 871
FT DOMAIN 52 92
FT DOMAIN 93 136
FT CARBOHYD 127 127
FT CARBOHYD 233 233
FT CARBOHYD 289 289
FT CARBOHYD 425 425
FT CARBOHYD 533 533
FT CARBOHYD 590 590
SQ SEQUENCE 871 AA; 99487 MW; 80848F81071F70AA CRC64;

Query Match 86.8%; Score 66; DB 1; Length 871;
Best Local Similarity 91.7%; Pred. No. 0.001;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
DB 196 MRPVYPTKTFPN 207
||| :||:|||||

RESULT 4
YEB6_YEAST STANDARD; PRT; 493 AA.
ID YEB6_YEAST
AC P39997;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOHETICAL 57.4 KDA PROTEIN IN PMP2-VAC8 INTERGENIC REGION.
GN YEL016C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO YEAST YCR26C.
CC -----
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CC -----
DR EMBL; X59720; CAA42318.1; -
DR PIR; S19437; S19437.
DR PIR; S27380; S27380.
DR SGD; S0000621; YCR026C.
DR InterPro; IPR002591; -
DR Pfam; PF01663; Phosphodiester; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 114 135 POTENTIAL.
SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

Query Match 65.8%; Score 50; DB 1; Length 743;
Best Local Similarity 61.5%; Pred. No. 0.47;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
DB 210 FMIPSPTPTTFPN 222
||| :||:||||

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RESULT 6
E13E_HORVU STANDARD; PRT; 316 AA.
AC Q02438;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE GV (EC 3.2.1.39) ((1->3)-BETA-GLUCAN
DE ENDOHYDROLASE GV) ((1->3)-BETA-GLUCANASE ISOENZYME GV) (BETA-1,3-
DE ENDOGLUCANASE GV).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
OC Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, CLIPPER; TISSUE=Root, and Leaf;
RX MEDLINE=94307426; PubMed=8034043;
RA Xu P., Harvey A.J., Fincher G.B.;
RT "Heterologous expression of cDNAs encoding barley (Hordeum vulgare)
RT (1->3)-beta-glucanase isoenzyme GV.";
RL FEBS Lett. 348:206-210(1994).
RN [2]
RP SEQUENCE OF 5-316 FROM N.A.
RC STRAIN=CV, CLIPPER; TISSUE=Root, and Leaf;
RX MEDLINE=93013030; PubMed=1398132;
RA Xu P., Wang J., Fincher G.B.;
RT "Evolution and differential expression of the (1->3)-beta-glucan
RT endohydrolase-encoding gene family in barley, Hordeum vulgare.";
RL Gene 120:157-165(1992).
CC -!- FUNCTION: MAY PROVIDE A DEGREE OF PROTECTION AGAINST MICROBIAL
CC INVASION OF GERMINATED BARLEY GRAIN THROUGH ITS ABILITY TO DEGRADE
CC FUNGAL CELL WALL POLYSACCHARIDES.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,3-BETA-D-GLUCOSIDIC LINKAGES
CC IN 1,3-BETA-D-GLUCANS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -!- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
EMBL; M96939; AAA21564.1; -.
DR F1R; JCI438; JCI438.
DR HSSP; P15737; IGHS.
DR InterPro; IPR000490; -.
DR Pfam; PF00332; Glyco_hydro_17; 1.
DR PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
KW Hydrolase; Glycosidase; Multigene family.
FT ACT_SITE 239 239 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 296 296 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 316 AA; 34413 MW; OCC0AAA9D48269B4F CRC64;

Query Match 58.6%; Score 44.5; DB 1; Length 316;
Best Local Similarity 81.8%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 RPYVPTKTFN 13
DB 307 QPYPT-TFN 316
:|||||
RT pigment complex, crustacyanin.;
RA Findlay J.B.C.;
RX MEDLINE=91224133; PubMed=2026162;
RA Keen J.N., Caceres I., Eliopoulos E.E., Zagalsky P.F.,
RA "Complete sequence and model for the A2 subunit of the carotenoid
RT pigment complex, crustacyanin.";
RL Eur. J. Biochem. 197:407-417(1991).
CC -!- FUNCTION: BINDS THE CAROTENOID ASTAXANTHIN WHICH PROVIDES THE BLUE
CC COLORATION TO THE CARAPACE OF THE LOBSTER.
CC -!- SUBUNIT: OLIGOMER: CAN FORM DIMERS (BETA-CRUSTACYANIN); OR
CC COMPLEXES OF 16 SUBUNITS (ALPHA-CRUSTACYANIN). THERE ARE FIVE
CC TYPES OF SUBUNITS: A1, A2, A3, C1 AND C2.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR, CARAPACE.

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
GN LACZ OR LACA.
OS Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Thermoanaerobacter group; Thermoanaerobacter.
OX NCBI_TaxID=1757;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33223 / 39E;
RA Zverlov V.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
EMBL; Y08557; CAA69850.1; -.
DR InterPro; IPR001649; -.
DR Pfam; PF00703; Glyco_hydro_2; 1.
DR PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
DR PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
KW Hydrolase; Glycosidase.
FT ACT_SITE 388 388 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 453 453 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 743 AA; 85796 MW; FE011FE517E51DFC CRC64;

Query Match 55.3%; Score 42; DB 1; Length 743;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFN 13
DB 454 YNGHMYPTKSYDN 466
:|||||
RT Complete sequence and model for the A2 subunit of the carotenoid
RA Findlay J.B.C.;
RX MEDLINE=91224133; PubMed=2026162;
RA Keen J.N., Caceres I., Eliopoulos E.E., Zagalsky P.F.,
RA "Complete sequence and model for the A2 subunit of the carotenoid
RT pigment complex, crustacyanin.";
RL Eur. J. Biochem. 197:407-417(1991).
CC -!- FUNCTION: BINDS THE CAROTENOID ASTAXANTHIN WHICH PROVIDES THE BLUE
CC COLORATION TO THE CARAPACE OF THE LOBSTER.
CC -!- SUBUNIT: OLIGOMER: CAN FORM DIMERS (BETA-CRUSTACYANIN); OR
CC COMPLEXES OF 16 SUBUNITS (ALPHA-CRUSTACYANIN). THERE ARE FIVE
CC TYPES OF SUBUNITS: A1, A2, A3, C1 AND C2.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR, CARAPACE.

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CC -!- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
 DR PIR: S15391; S15391.
 DR InterPro: IPR000566; -.
 DR InterPro: IPR002345; -.
 DR InterPro: IPR003057; -.
 DR Pfam: PF00061; Lipocalin; 1.
 DR PRINTS: PR00179; LIPOCALIN.
 DR PRINTS: PR01273; INVERTCOLOR.
 DR PROSITE: PS00213; LIPOCALIN; 1.
 KW Pigment; Lipocalin; Transport.
 FT DISULFID 12 119 BY SIMILARITY.
 FT DISULFID 46 170 BY SIMILARITY.
 SQ SEQUENCE 174 AA; 19670 MW; AC47FAA650C5E44E CRC64;

Query Match 52.6%; Score 40; DB 1; Length 174;
 Best Local Similarity 87.5%; Pred. No. 5.2;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 VYPTKTFP 12
 ||||| ||
 Db 80 VYPTKEFP 87

RESULT 9

MD21_HUMAN
 ID MD21_HUMAN STANDARD; PRT; 205 AA.
 AC Q13257;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1)
 DE (HSMAD2).
 GN MAD2L1 OR MAD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=96421709; PubMed=8824189;
 RA Li Y., Benezra R.;
 RT "Identification of a human mitotic checkpoint gene: hsmad2.";
 RL Science 274:246-248(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jin D.-Y., Jeang K.-T.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kleibert S., Barnikol-Watanabe S., Kratzin H.D., Hilschmann N.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP INTERACTION WITH CDC20.
 RP MEDLINE=98301442; PubMed=9637688;
 RA Fang G., Yu H., Kirschner M.W.;
 RT "The checkpoint protein MAD2 and the mitotic regulator CDC20 form a
 RT ternary complex with the anaphase-promoting complex to control
 RT anaphase initiation.";
 RL Genes Dev. 12:1871-1883(1998).
 RN [5]
 RP INTERACTION WITH ADAM17.
 RP PubMed=10527948;
 RA Nelson K.K., Schlondorff J., Blobel C.P.;
 RT "Evidence for an interaction of the metalloprotease-disintegrin tumour
 RT necrosis factor alpha convertase (TACE) with mitotic arrest deficient
 RT 2 (MAD2), and of the metalloprotease-disintegrin MDC9 with a novel
 RT MAD2-related protein, MAD2-beta.";
 RL Biochem. J. 343:673-680(1999).
 RN [6]
 RP STRUCTURE BY NMR OF 11-195.
 RP MEDLINE=20165182; PubMed=10700282;
 RA Luo X., Fang G., Coldiron M., Lin Y., Yu H., Kirschner M.W.,

RA Wagner G.;
 RT "Structure of the Mad2 spindle assembly checkpoint protein and its
 RT interaction with Cdc20.";
 RL Nat. Struct. Biol. 7:224-229(2000).
 CC -!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT
 CC WHICH MONITORS THE PROCESS OF KINETOCORE-SPINDLE ATTACHMENT AND
 CC DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT
 CC INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY
 CC SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
 CC METAPHASE PLATE.
 CC -!- SUBUNIT: INTERACTS WITH CDC20 AND WITH ADAM17 (TACE).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- SIMILARITY: BELONGS TO THE MAD2 FAMILY.

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EMBL; U65410; AAC50781.1; -.
 DR EMBL; U31278; AAC52060.1; -.
 DR EMBL; AJ000186; CAA03943.1; -.
 DR MIM; 601467; -.
 DR PDB; 1DUJ; 08-MAR-00.
 DR InterPro: IPR003511; -.
 DR Pfam: PF02301; HORNA; 1.
 KW Cell cycle; Mitosis; Nuclear protein; 3D-structure.
 SQ SEQUENCE 205 AA; 23510 MW; B8DCBF0043836784 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 205;
 Best Local Similarity 54.5%; Pred. No. 6.2;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YMRPVYPTKTF 11
 | | : | : | : |
 Db 33 YQGIYPTSETF 43

RESULT 10

MD21_MOUSE
 ID MD21_MOUSE STANDARD; PRT; 205 AA.
 AC Q9Z1B5; Q9J153;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1).
 GN MAD2L1 OR MAD2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Embryo;
 RA Jin D.-Y., Jeang K.-T.;
 RT "Identification of a novel component of the spindle assembly
 RT checkpoint in mammalian cells.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX PubMed=10892650;
 RA Dobles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;
 RT "Chromosome missegregation and apoptosis in mice lacking the mitotic
 RT checkpoint protein Mad2.";
 RL Cell 101:645-645(2000).
 CC -!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT
 CC WHICH MONITORS THE PROCESS OF KINETOCORE-SPINDLE ATTACHMENT AND
 CC DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT

```
CC INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY
CC SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
CC METAPHASE PLATE (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH CDC20.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
CC -----
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CC -----
DR EMBL; U83902; AAD09238.1; -.
DR EMBL; AF261919; AAF69525.1; -.
DR InterPro: IPR003511; -.
DR Pfam; PF02301; HORMA; 1.
KW Cell cycle; Micros; Nuclear protein.
FT CONFLICT 157 157 T -> A (IN REF. 1).
FT CONFLICT 178 178 C -> S (IN REF. 1).
FT CONFLICT 201 201 T -> I (IN REF. 1).
FT SEQUENCE 205 AA; 23598 MW; A9F3F28BC4C9738E CRC64;
SQ
Query Match 52.6%; Score 40; DB 1; Length 205;
Best Local Similarity 54.5%; Pred. No. 6.2;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 YMRPVPTKTF 11
DB 33 YQGIYPSETF 43
| | :|:|:|
| | :|:|:|

RESULT 11
CYSL_YCES
ID CYSL_YCES STANDARD; PRT; 346 AA.
AC P20721;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LOW-TEMPERATURE-INDUCED CYSTEINE PROTEINASE PRECURSOR (EC 3.4.22.-)
DE (FRAGMENT).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, VFNT CHERRY;
RA Schaffer M.A., Fischer R.L.;
RT "Analysis of mRNAs that accumulate in response to low temperature
RT identifies a thiolprotease in tomato.";
RL Plant Physiol. 87:431-436(1988).
CC -1- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
CC PAININ FAMILY OF THIOL PROTEASES.
CC -----
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CC -----
DR EMBL; M21444; AAA66308.1; -.
DR PIR; JA0159; JA0159.
DR HSSP; P00785; 2ACT.
DR MEROPS; C01.029; -.
DR InterPro: IPR000118; -.
Query Match 52.6%; Score 40; DB 1; Length 1547;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
DR InterPro: IPR000169; -.
DR InterPro: IPR000668; -.
DR Pfam; PF00112; Peptidase_C1; 1.
DR Pfam; PF00396; granulin; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
KW Hydrolase; Thiol protease; zymogen; Glycoprotein.
FT NON_TER 1 1
FT PROPEP <1 17 ACTIVATION PEPTIDE (POTENTIAL).
FT CHAIN 18 346 LOW-TEMPERATURE-INDUCED CYSTEINE
FT PROTEINASE.
FT ACT_SITE 42 42 BY SIMILARITY.
FT ACT_SITE 178 178 BY SIMILARITY.
FT ACT_SITE 198 198 BY SIMILARITY.
FT DISULFID 39 81 BY SIMILARITY.
FT DISULFID 73 114 BY SIMILARITY.
FT DISULFID 172 223 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 346 AA; 37429 MW; D42AC73944010928 CRC64;
Query Match 52.6%; Score 40; DB 1; Length 346;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 MRPVPTKTFN 13
DB 227 IEPSYVKTGPN 238
| | :|:|:|
| | :|:|:|

RESULT 12
RRPO_PMV
ID RRPO_PMV STANDARD; PRT; 1547 AA.
AC P20951;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICATION PROTEIN (176 KDA PROTEIN) (ORF 1) [CONTAINS: RNA-
DE DIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].
OS Papaya mosaic potexvirus (PMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12181;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89381685; PubMed=2778435;
RA Sit T.L., Abouhaider M.G., Holy S.;
RT "Nucleotide sequence of papaya mosaic virus RNA.";
RL J. Gen. Virol. 70:2325-2331(1989).
CC -1- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
CC POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
CC -----
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CC -----
DR EMBL; D13957; BAA03050.1; -.
DR PIR; JQ0096; JQ0096.
DR InterPro: IPR000606; -.
DR Pfam; PF01443; Viral_helicase1; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW Transferase.
FT NP_BIND 822 829 ATP (POTENTIAL).
SQ SEQUENCE 1547 AA; 176320 MW; 6CA4282C6A082622 CRC64;
Query Match 52.6%; Score 40; DB 1; Length 1547;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 YPTKTFPN 13
Db 409 YPTKTFDN 416

RESULT 13
HMD2_SOLTU STANDARD; PRT; 595 AA.
AC Q41437;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 2 (EC 1.1.1.34) (HMG-
COA REDUCTASE 2) (HMG2.2).
GN HMG2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, KENNEBEC; TISSUE=Tuber;
RX MEDLINE=97201488; PubMed=9049274;
RA Korth K.L., Sterner B.A., Bhattacharyya M.K., Dixon R.A.;
RT "HMG-CoA reductase gene families that differentially accumulate
transcripts in potato tubers are developmentally expressed in floral
tissues.";
RT Plant Mol. Biol. 33:545-551(1997).
RL
CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF MEVALONATE. THE SPECIFIC
PRECURSOR OF ALL ISOPRENOID COMPOUNDS PRESENT IN PLANTS.
CC -1- CATALYTIC ACTIVITY: (R)-MEVALONATE + COA + 2 NADP(+) = (S)-3-
HYDROXY-3-METHYLGLUTARYL-COA + 2 NADPH.
CC -1- PATHWAY: MEVALONATE BIOSYNTHESIS, PLANT ISOPRENOID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
RETICULUM.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN YOUNG FLOWERS AND IN MATURE
SEEDS AND OVARIES.
CC -1- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.
CC
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CC
DR EMBL; U51985; AAB52551.1; -
DR Mendel; 10574; Soltu; 1091:10574.
DR InterPro; IPR002202; -
DR Pfam; PF00368; HMG-CoA_red; 1.
DR PRINTS; PR00071; HMGCOARDTASE.
DR PROSITE; PS00066; HMG_COA_REDUCTASE_1; 1.
DR PROSITE; PS00318; HMG_COA_REDUCTASE_2; 1.
DR PROSITE; PS01192; HMG_COA_REDUCTASE_3; 1.
DR PROSITE; PS50065; HMG_COA_REDUCTASE_4; 1.
KW Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane;
KW Isoprene biosynthesis; NADP; Multigene family.
FT DOMAIN 1 112 MEMBRANE-BOUND (BY SIMILARITY).
FT DOMAIN 113 183 LINKER (BY SIMILARITY).
FT DOMAIN 184 595 CATALYTIC (BY SIMILARITY).
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT ACT_SITE 278 278 BY SIMILARITY.
FT ACT_SITE 486 486 BY SIMILARITY.
FT ACT_SITE 584 584 GENERAL BASE (BY SIMILARITY).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 342 342 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 588 588 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 595 AA; 63841 MW; 0FA7069849D41D57 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 890;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 RPVYPTKTFP 12
Db 650 RPVYSVKLFP 659

RESULT 15
KINI_YEAST STANDARD; PRT; 1064 AA.
AC P13185; Q04606;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROTEIN KINASE KINI (EC 2.7.1.-).
GN KINI OR YDR122W OR YD9727.17.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
```

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OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87317589; PubMed=2957690;
RA Levin D.E., Hammond C.I., Ralston R.O., Bishop J.M.;
RT "Two yeast genes that encode unusual protein kinases.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6035-6039(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Murphy L., Shore L., Harris D., Barrell B.G., Rajandream M.A.,
RA Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A SERINE/THREONINE PROTEIN
CC KINASE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC NIM1 SUBFAMILY.
CC -----
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CC -----
DR EMBL; MG9017; AAA34722.1; -.
DR EMBL; Z48758; CAA88675.1; -.
DR PIR; S42438; S42438.
DR HSP; O63450; IA06.
DR SGD; S0002529; KIN1.
DR InterPro; IPR000719; -.
DR InterPro; IPR002290; -.
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 120 398
FT NP_BIND 126 134 ATP (BY SIMILARITY).
FT BINDING 149 149 ATP (BY SIMILARITY).
FT ACT_SITE 269 269 BY SIMILARITY.
FT CONFLICT 25 25 S -> R (IN REF. 1).
FT CONFLICT 453 453 T -> H (IN REF. 1).
FT CONFLICT 455 455 V -> G (IN REF. 1).
FT CONFLICT 718 718 A -> R (IN REF. 1).
FT CONFLICT 920 921 NI -> IN (IN REF. 1).
FT CONFLICT 976 976 T -> A (IN REF. 1).
FT CONFLICT 979 980 SI -> T (IN REF. 1).
FT CONFLICT 984 985 KT -> NS (IN REF. 1).
SQ SEQUENCE 1064 AA; 120070 MW; E4104B84A8E45C36 CRC64;
```

```
Query Match 51.3%; Score 39; DB 1; Length 1064;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 YMRPVYPTKTFP 12
    |||||  |  :|
Db 802 YMRPPMPSSAYP 813
```

Search completed: July 19, 2001, 14:47:09
Job time: 171 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:46:48 ; Search time 42.51 Seconds
(without alignments)
40.460 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213

Perfect score: 76

Sequence: 1 YMRPVYPTKTFPN 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_rodent:*
13: sp_unclassified:*
14: sp_vertebrate:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	76	100.0	862	11	Q9R1E6
2	76	100.0	863	4	Q13822
3	76	100.0	863	4	Q15117
4	76	100.0	915	4	Q13827
5	70	92.1	885	11	Q64610
6	69	90.8	257	11	Q88827
7	69	90.8	845	4	Q9NP23
8	69	90.8	925	4	Q9P1P6
9	68	89.5	875	11	P97675
10	68	89.5	876	11	P70641
11	65	85.5	875	4	Q14638
12	65	85.5	875	11	Q63490
13	65	85.5	875	11	P97676
14	64	84.2	32	6	Q9TRD2
15	64	84.2	817	14	O90761
16	64	84.2	817	14	O925H1
17	49	64.5	457	10	Q9S082
18	49	64.5	461	10	Q9S081
19	49	64.5	829	5	P90754

20	48	63.2	479	10	Q9FS13
21	48	63.2	496	10	Q9S083
22	47	61.8	479	10	Q42974
23	45	59.2	674	5	P90755
24	43	56.6	173	4	Q9Y5A0
25	43	56.6	343	3	Q9UUN9
26	43	56.6	401	4	Q9HAC9
27	43	56.6	757	11	Q9WVC8
28	42	55.3	429	2	O69013
29	42	55.3	1004	5	O69013
30	41	53.9	247	5	O44145
31	41	53.9	381	5	O9XUV4
32	41	53.9	427	10	Q43423
33	41	53.9	433	2	Q9PAB9
34	41	53.9	453	4	Q9Y6X5
35	41	53.9	493	10	O22499
36	41	53.9	1829	5	Q22248
37	40	52.6	203	13	P79935
38	40	52.6	247	10	Q9SN23
39	40	52.6	291	10	Q9M4F6
40	40	52.6	307	5	O61478
41	40	52.6	430	5	Q9NB54
42	40	52.6	466	10	O49877
43	40	52.6	2066	14	P89920
44	40	52.6	3579	5	Q9V5N8
45	39	51.3	157	5	Q9Y0E8

ALIGNMENTS

RESULT 1

Q9R1E6 PRELIMINARY; PRT; 862 AA.
ID Q9R1E6
AC Q9R1E6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE (BC 3.1.4.1).
GN NPPS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B/6;
RA Sano K., Piao J.-H.;
RT "Cloning and chromosomal assignment of mouse phosphodiesterase
RT I/nucleotide pyrophosphatase (PD-I alpha/autotaxin).";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF123542; RAD46480.1;
DR InterPro: IPR001212;
DR InterPro: IPR002591;
DR Pfam: PF01033; Somatomedin_B; 2.
DR Pfam: PF01663; Phosphodiesterase; 1.
DR PRINTS: PR00022; SOMATOMEDINB.
DR PROSITE: PS00524; SOMATOMEDIN_B; 2.
DR SMART: SM00201; SO; 1.
KW Hydrolase.
SQ SEQUENCE 862 AA; 98918 MW; 641F8F1443E4F8B0 CRC64;

Query Match 100.0%; Score 76; DB 11; Length 862;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13

Db 200 YMRPVYPTKTFPN 212

RESULT 2


```
Q13822
ID Q13822 PRELIMINARY; PRT; 863 AA.
AC Q13822;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE AUTOTAXIN-T.
GN ATX-T.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=95074054; PubMed=7982964;
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,
RA Sobel M.E., Liotta L.A., Stracke M.L.;
RT "cDNA cloning of the human tumor motility-stimulating protein,
RT autotaxin, reveals a homology with phosphodiesterases.";
RL J. Biol. Chem. 269:30479-30484(1994).
RN EMBL: L46720; AAB00855.1; -;
DR InterPro; IPR001212; -;
DR InterPro; IPR001604; -;
DR InterPro; IPR002591; -;
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PR00022; SOMATOMEDINB.
DR SMART; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 863 AA; 99017 MW; F960DCE51663BABC CRC64;

Query Match 100.0%; Score 76; DB 4; Length 863;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | | | |
Db 201 YMRPVYPTKTFPN 213

RESULT 3
Q15117
ID Q15117 PRELIMINARY; PRT; 863 AA.
AC Q15117;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I ALPHA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96163899; PubMed=8586446;
RA Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J.,
RA Nakamura H., Sano K.;
RT "Molecular cloning and chromosomal assignment of the human brain-type
RT phosphodiesterase I/nucleotide pyrophosphatase gene (PDNP2).";
RL Genomics 30:380-384(1995).
DR EMBL: D45421; BAA08260.1; -;
DR InterPro; IPR001212; -;
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DR InterPro; IPR001604; -;
DR InterPro; IPR002591; -;
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PR01663; Phosphodiect; 1.
DR PROSITE; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 863 AA; 99040 MW; 318EA28BICEA7A55 CRC64;

Query Match 100.0%; Score 76; DB 4; Length 863;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | | | |
Db 201 YMRPVYPTKTFPN 213

RESULT 4
Q13827
ID Q13827 PRELIMINARY; PRT; 915 AA.
AC Q13827;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE AUTOTAXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TUMOR;
RX MEDLINE=95074054; PubMed=7982964;
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,
RA Sobel M.E., Liotta L.A., Stracke M.L.;
RT "cDNA cloning of the human tumor motility-stimulating protein,
RT autotaxin, reveals a homology with phosphodiesterases.";
RL J. Biol. Chem. 269:30479-30484(1994).
DR EMBL: L35594; AAA64785.1; -;
DR InterPro; IPR001212; -;
DR InterPro; IPR001604; -;
DR InterPro; IPR002591; -;
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64;

Query Match 100.0%; Score 76; DB 4; Length 915;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | | | |
Db 201 YMRPVYPTKTFPN 213

RESULT 5
Q64610
ID Q64610 PRELIMINARY; PRT; 885 AA.
AC Q64610;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I (EC 3.1.4.1).
GN NPH-TYPE III
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=95050605; PubMed=7961762;
RA Narita M., Goli J., Nakamura H., Sano K.;
RT "Molecular cloning, expression, and localization of a brain-specific
FT phosphodiesterase I/nucleotide pyrophosphatase (PD-I alpha) from rat
RT brain.";
RL J. Biol. Chem. 269:28235-28242(1994).
DR EMBL; D28560; BAA05910.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
KW Hydrolase.
SQ SEQUENCE 885 AA; 101309 MW; 8C5C0AFC52007973 CRC64;

Query Match 92.1%; Score 70; DB 11; Length 885;
Best Local Similarity 92.3%; Pred. No. 0.00065;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
   | | | | | | | | | |
Db 198 YTRPVYPTKTFPN 210

RESULT 6
O88827
ID O88827 PRELIMINARY; PRT; 257 AA.
AC O88827
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PLASMA CELL MEMBRANE GLYCOPROTEIN (FRAGMENT).
GN PCL
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakoda H., Asano T., Ogiwara T.;
RT "N terminal of the plasma cell membrane glycoprotein PC-1.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017596; BAA33393.1; -
DR InterPro; IPR001212; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00201; SO; 1.
FT NON_TER 257 257
SQ SEQUENCE 257 AA; 28306 MW; CF348E474FBDAFED CRC64;

Query Match 90.8%; Score 69; DB 11; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
   | | | | | | | | | |
Db 230 MRPVYPTKTFPN 241

RESULT 7
Q9NP23
ID Q9NP23 PRELIMINARY; PRT; 845 AA.
AC Q9NP23
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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE D3131F15.2 (PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE.1
DE (HOMOLOGOUS TO MOUSE LV-41 ANTIGEN) (PCL, NPPS)) (FRAGMENT).
GN PDPN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peck A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117378; CAB99365.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
FT NON_TER 1
SQ SEQUENCE 845 AA; 96844 MW; C2DD58248BDAC52E CRC64;

Query Match 90.8%; Score 69; DB 4; Length 845;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
   | | | | | | | | | |
Db 168 MRPVYPTKTFPN 179

RESULT 8
Q9P1P6
ID Q9P1P6 PRELIMINARY; PRT; 925 AA.
AC Q9P1P6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PDPN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rozzali M., Pizzuti A., Trischitta E.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110304; AAF36094.1; -
DR EMBL; AF110280; AAF36094.1; JOINED.
DR EMBL; AF110281; AAF36094.1; JOINED.
DR EMBL; AF110283; AAF36094.1; JOINED.
DR EMBL; AF110284; AAF36094.1; JOINED.
DR EMBL; AF110285; AAF36094.1; JOINED.
DR EMBL; AF110286; AAF36094.1; JOINED.
DR EMBL; AF110287; AAF36094.1; JOINED.
DR EMBL; AF110288; AAF36094.1; JOINED.
DR EMBL; AF110289; AAF36094.1; JOINED.
DR EMBL; AF110290; AAF36094.1; JOINED.
DR EMBL; AF110291; AAF36094.1; JOINED.
DR EMBL; AF110292; AAF36094.1; JOINED.
DR EMBL; AF110293; AAF36094.1; JOINED.
DR EMBL; AF110294; AAF36094.1; JOINED.
DR EMBL; AF110295; AAF36094.1; JOINED.
DR EMBL; AF110296; AAF36094.1; JOINED.
DR EMBL; AF110297; AAF36094.1; JOINED.
DR EMBL; AF110298; AAF36094.1; JOINED.
DR EMBL; AF110299; AAF36094.1; JOINED.
DR EMBL; AF110300; AAF36094.1; JOINED.
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DR	EMBL; AF110301; AAF36094.1; JOINED.
DR	EMBL; AF110302; AAF36094.1; JOINED.
DR	EMBL; AF110303; AAF36094.1; JOINED.
DR	InterPro: IPR001212; -
DR	InterPro: IPR001604; -
DR	InterPro: IPR002591; -
DR	Pfam: PF01033; Somatomedin_B; 2.
DR	Pfam: PF01663; Phosphodiester_1.
DR	PRINTS; PR0022; SOMATOMEDINB.
DR	PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR	SMART; SM00477; NUC; 1.
SQ	SEQUENCE 925 AA; 104924 MW; 05BC

RESULT	9
ID	P97675 PRELIMINARY; PRT; 875 AA.
AC	P97675;
DT	01-MAY-1997 (TrEMBLrel. 03, Created)
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	ALKALINE PHOSPHODIESTERASE.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;	
[1]	
RP	SEQUENCE FROM N.A.
KC	STRAIN=SPRAGUE-DAWLEY;
RX	MEDLINE=97250972; PubMed=9096610;
RA	Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W., Maurice M.;
RT	"Biochemical and molecular identification of distinct forms of alkaline phosphodiesterase I expressed on the apical and basolateral plasma membrane surfaces of rat hepatocytes.";
RL	Hepatology 25:995-1002(1997).
DR	ENBL; U78787; AAB61535.1; -.
DR	InterPro; IPR001212; -.
DR	InterPro; IPR001604; -.
DR	InterPro; IPR002591; -.
DR	Pfam; PF01033; Somatomedin_B; 2.
DR	Pfam; PF01663; Phosphodiect; 1.
DR	PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR	SMART; SM00477; NUC; 1.
SQ	SEQUENCE 875 AA; 99166 MW; 8FEB9A482173D377 CRC64;

RESULT 10	
P70641	
ID	P70641
AC	P70641; PRELIMINARY; PRT; 876 AA.
DT	01-FEB-1997 (TRMBLrel. 02, Created)
DT	01-FEB-1997 (TRMBLrel. 02, Last sequence update)
DT	01-MAR-2001 (TRMBLrel. 16, Last annotation update)
DE	PHOSPHODIESTERASE I.

OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE, PROXIMAL;
RA	Sano K.;
RT	"Molecular cloning of phosphodiesterase I cDNA from rat small intestine.";
RT	Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RL	EMBL; D30649; BAA06333.1; -;
DR	InterPro; IPR001212; -;
DR	InterPro; IPR001604; -;
DR	InterPro; IPR002591; -;
DR	Pfam; PF01033; Somatomedin_B; 2.
DR	Pfam; PF01663; Phosphodiester; 1.
DR	PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR	SMART; SM00477; NUC; 1.
SQ	SEQUENCE 876 AA; 99328 MW; D3F772C34A0C437A CRC64;

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RESULT 11
ID 014638
ID 014638 PRELIMINARY; PRT; 875 AA.
DT AC
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE BETA (EC 3.1.4.1)
DE (PHOSPHODIESTERASE I BETA).
GN PDNP3.
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=PROSTATE;
RC MEDLINE=98008933; PubMed=9344668;
RA Piao J.-H., Goding J.W., Nakamura H., Sano K.;
RT "Molecular cloning and chromosomal localization of PD-IBeta (PDNFB), a
RL new member of the human phosphodiesterase I genes.";
RL Genomics 45:412-415(1997).
RN [2]
RN SEQUENCE OF 189-875 FROM N.A.
RA Hou S., Wohlmann P., Le T.;
RT "The sequence of Homo sapiens PAC clone DJ0988G15."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE OF 189-875 FROM N.A.
RA Waterston R.H.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 189-875 FROM N.A.
RA Waterston R.H.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE OF 189-875 FROM N.A.
RA Waterston R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005632; AAC51813.1; -.
DR EMBL; AC005587; AAD05192.1; -.
DR InterPro; IPR001212; -.

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DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase I; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
DR KW Hydrolase.
SQ SEQUENCE 875 AA; 100096 MW; 329CF41667497BC4 CRC64;

Query Match 85.5%; Score 65; DB 4; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
   ||| :|||||||
Db 196 YMRAMYPTKTFPN 208

RESULT 12
ID Q63490 PRELIMINARY; PRT; 875 AA.
AC Q63490;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RB13-6 ANTIGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAQUE-DAWLEY; TISSUE=BRAIN;
RA MEDLINE=95247775; PubMed=7730366;
RX Deissler H., Lottspeich F., Rajewsky M.F.;
RT "Affinity purification and cDNA cloning of rat neural differentiation
RT and tumor cell surface antigen gp130RB13-6 reveals relationship to
RT human and murine PC-1."
RL J. Biol. Chem. 270:9849-9855(1995).
DR EMBL; Z47987; CAA88029.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase I; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 875 AA; 99087 MW; 98A9FBFF82DFBA6 CRC64;

Query Match 85.5%; Score 65; DB 11; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
   ||| :|||||||
Db 197 YMRAMYPTKTFPN 209

RESULT 13
ID P97676 PRELIMINARY; PRT; 875 AA.
AC P97676;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=97250927; PubMed=9096610;
RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.,
RA Maurice M.;
RT "Biochemical and molecular identification of distinct forms of
RT alkaline phosphodiesterase I expressed on the apical and basolateral
RT plasma membrane surfaces of rat hepatocytes."
RL Hepatology 25:995-1002(1997).
DR EMBL; U78788; AAB61536.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase I; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00201; SO; 1.
SQ SEQUENCE 875 AA; 99071 MW; 4205F263E8A933EA CRC64;

Query Match 85.5%; Score 65; DB 11; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
   ||| :|||||||
Db 197 YMRAMYPTKTFPN 209

RESULT 14
Q9TRD2 PRELIMINARY; PRT; 32 AA.
ID Q9TRD2 PRELIMINARY; PRT; 32 AA.
AC Q9TRD2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 260 KDA MAJOR ACIDIC FIBROBLAST GROWTH FACTOR-STIMULATED
DE PHOSPHOPROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=94086550; PubMed=7505270;
RA Oda Y., Kuo M.D., Huang S.S., Huang J.S.;
RT "The major acidic fibroblast growth factor (aFGF)-stimulated
RT phosphoprotein from bovine liver plasma membranes has aFGF-stimulated
RT kinase, autoadenylation, and alkaline nucleotide phosphodiesterase
RT activities."
RL J. Biol. Chem. 268:27318-27326(1993).
SQ SEQUENCE 32 AA; 3699 MW; 5CCFFA9EB55E6927 CRC64;

Query Match 84.2%; Score 64; DB 6; Length 32;
Best Local Similarity 91.7%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MRPVYPTKTFPN 13
   ||||| |||
Db 2 MRPVYPTKTFPN 13

RESULT 15
O90761 PRELIMINARY; PRT; 817 AA.
ID O90761 PRELIMINARY; PRT; 817 AA.
AC O90761;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-
DE NUCLEOTIDE PHOSPHODIESTERASE).
GN PCL.
OS Fowlpox virus.
```

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OX Avipoxvirus.
 NCBI_TaxID=10261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FP-9;
 RX MEDLINE=98325194; PubMed=9658122;
 RA Laidlaw S.M., Anwar M.A., Thomas W., Green P., Shaw K., Skinner M.A.;
 RT "Fowlpox virus encodes nonessential homologs of cellular alpha-SNAP,
 PC-1, and an orphan human homolog of a secreted nematode protein.";
 RL J. Virol. 72:6742-6751(1998).
 CC -1- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 CC OLIGO-NUCLEOTIDES.
 DR EMBL; AJ006408; CAA07014.1; -.
 DR InterPro; IPR001604; -.
 DR InterPro; IPR002591; -.
 DR Pfam; PF01663; Phosphodiester; 1.
 DR SMART; SM00477; NUC; 1.
 KW Hydrolase.
 SQ SEQUENCE 817 AA; 94004 MW; CB68DA0508CC568E CRC64;

Query Match 84.2%; Score 64; DB 14; Length 817;
 Best Local Similarity 91.7%; Pred. No. 0.0066;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 MRPVYPTKTFPN 13
 Db 155 MRPVYPTNTFPN 166
 ||||| |||||

Search completed: July 19, 2001, 14:46:49
 Job time: 172 sec